

GenCore version 5.1.7
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OM nucleic - protein search, using frame_plus_nzp model

Run on: February 1, 2006, 13:19:06 ; Search time 53.4986 Seconds
(without alignments)
2961.978 Million cell updates/sec

Title: us-09-888-264-1
Perfect score: 1 ccgagggccatgagtcgagc.....ccatcgaggaccatcaaa 1123
Sequence:

Scoring table:
BLASTSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 4332886

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+nzp.model -DEV=xlp
-O=/abses/ABSSWEB.spool/US09888264/runat 01022006 131838 14779/app query.fasta_1
-DB=uniprot -QPM=faetan -SUFFIX=rip -MINMATCH=0.1 -LOOFC=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCLION=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPM=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abses02p
-USER=US09888264 @CGN 1.1 580 @runat 01022006 131838 14779 -NCPU=6 -ICPU=3
-NO MAP -MGC SCORES=0 -WAIT -DSPBLCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THRAIDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Uniprot 05.80: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1600	73.4	314	061BH0_HUMAN	Q61bh0 homo sapien
2	1600	73.4	314	Q5RFR5_PONPY	Q5rfj5 pongo pygma
3	1595	73.1	313	M20M_HUMAN	Q02978 homo sapien
4	1558	71.4	314	Q5SX53_MOUSE	Q5sx53 mus musculu
5	1553	71.2	313	M20M_MOUSE	Q5c62 mus musculu
6	1549	71.0	314	Q5E9W4_BOVIN	Q5E9W4 bos taurus
7	1544	70.8	313	M20M_BOVIN	P22292 bos taurus
8	1535	70.4	313	M20M_RAT	P97700 rattus norv
9	1418	65.0	305	Q566L1_XENTR	Q566L1 xenopus tro
10	1407	64.5	305	Q61NH3_XENLA	Q61nh3 xenopus lae
11	1382	63.4	308	Q61Q89_BRARE	Q61q89 brachydanto
12	1363	62.5	313	Q4TA26_TETNG	Q4ta26 tetradodon n
13	1258	57.7	302	Q9CTC7_MOUSE	Q9ctc7 mus musculu
14	1064	48.8	307	Q61OH3_CABBR	Q61oh3 caenorhabdi
15	1052	48.2	306	P90992_CABEL	P90992 caenorhabdi
16	957	43.9	193	Q5SX46_MOUSE	Q5sx46 mus musculu

17	915.5	42.0	317	2	Q9VAJ9_DROME	Q9vaj9 drosophila
18	891.5	40.9	292	2	Q5TN06_ANOGA	Q5tn06 anopheles g
19	839.5	38.5	311	2	Q5VZ93_DROME	Q5vz93 drosophila
20	838.5	38.4	311	2	Q8XB4_DROME	Q8xb4 drosophila
21	782	35.9	301	2	Q9VZ94_DROME	Q9vz94 drosophila
22	716	32.8	318	2	Q54PY7_DICDI	Q54py7 dictyostell
23	608	27.9	309	2	Q53PA7_ORYSA	Q53pa7 oryza sativ
24	606	27.8	307	2	Q66PW8_SACOF	Q66pw8 saccharum o
25	602.5	27.6	302	2	Q42422_PANMI	Q42422 panicum mil
26	598	27.4	302	2	Q40918_PANMI	Q40918 panicum mil
27	597	27.4	299	2	Q6T871_PROSI	Q6t871 citrus jun
28	596	27.3	313	2	Q59IV3_MESCR	Q59iv3 mesembryant
29	596	27.3	321	2	Q6YX13_ORYSA	Q6yx13 oryza sativ
30	591	27.1	298	2	Q9CSM0_ARATH	Q9csm0 arabidopsis
31	590	27.1	308	2	Q8SF02_TOBAC	Q8sf02 nicotiana t
32	589	27.0	325	2	Q6EPX3_SACOF	Q6epx3 saccharum o
33	587	26.9	297	2	Q8SF04_TOBAC	Q8sf04 nicotiana t
34	587	26.9	306	2	Q60BY9_ORYSA	Q60ey9 oryza sativ
35	585	26.8	295	2	Q8SF03_TOBAC	Q8sf03 nicotiana t
36	585	26.8	297	2	Q9FSF4_TOBAC	Q9fsf4 nicotiana t
37	583	26.7	297	2	Q43649_SOLRU	Q43649 solanum tub
38	583	26.7	313	2	Q9SUT5_ARATH	Q9sjt5 arabidopsis
39	581	26.6	331	2	Q66PX4_SACOF	Q66px4 saccharum o
40	579	26.5	313	2	Q8LDF6_ARATH	Q8ldf6 arabidopsis
41	574	26.3	313	2	Q94K32_ARATH	Q94k32 arabidopsis
42	571.5	26.2	319	2	Q7RMU4_PLAYO	Q7rmu4 plasmodium
43	565.5	25.9	319	2	Q4XP74_PLACH	Q4xp74 plasmodium
44	561.5	25.7	319	2	Q4YBX9_PLABE	Q4ybx9 plasmodium
45	556	25.5	285	2	Q7QBN6_ANOGA	Q7qbn6 anopheles g

ALIGNMENTS

RESULT 1
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ID 061BH0_HUMAN PRELIMINARY; PRT; 314 AA.
AC 061BH0
AD 061BH0
DT 05-JUN-2004 (Trembl) 27, Created
DT 05-JUN-2004 (Trembl) 27, Last sequence update
DT 05-JUN-2004 (Trembl) 27, Last annotation update
DE SLIC25A11 protein.
DE SLIC25A11
GN Name=SLIC25A11;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR456834; CAC33115.1; -, mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
KW Transmembrane; Transport.
SQ SEQUENCE 314 AA; 34061 MW; 9D61F817089FF5AA CRC64;
Alignment Scores:
Pred. No.: 1,68e-106
Score: 1600.00
Percent Similarity: 100.0%
Best Local Similarity: 99.7%
Query Match: 73.4%
DB: 2
Length: 314
Matches: 313
Conservative: 1
Mismatch: 0
Indels: 0
Gaps: 0
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DB 1 MetAlaIatHrAlaSerAlaGlyAlaGlyIleApgGlyLysPforArghrSerPro 20

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QY 81 AAGTCCGTCAGAGTTCCTGTTTGGGGGCTGGCCGGATGGAGCTACAGTTTTCACG 140
DB 21 LysSerValLysPheLeuPheGlyGlyLeuAlaGlyMetGlyAlaThrValPheValGln 40
QY 141 CCCCTGAGCTGGTGAAGAAACCGGATGCACTTGAAGCGGGAGAGGGCCAAAGACTCGAAG 200
DB 41 ProLeuAspLeuValLysAsnArgMetGlnLeuSerGlyGlnGlyAlaThrValArgGln 60
QY 201 TACAAACACGAGCTTCATGCGCCCTCACAGATCTTGAAGCCAGAAAGCCCGAGGCGATT 260
DB 61 TyrLeuThrSerPheHisAlaLeuThrSerIleLeuValAlaGlnGlyLeuArgGlyIle 80
QY 261 TACACTGGGCTGTGGGCTGGCTGCTGGCTGAGGCGCACTTACACCACTACCCGCTTGGC 320
DB 81 TyrThrGlyLeuSerHisAlaGlyLeuLeuArgGlnAlaThrTyrThrThrThrArgLeuGly 100
QY 321 ATCTATACCGTGTGTTTGAAGCCCTGACTGGGGCTGATGTGTACTCCCTGGCTTTCG 380
DB 101 IleTyrThrValLeuPheGlnArgLeuThrGlyAlaAspGlyThrProProGlyPheLeu 120
QY 381 CTGAAGGCTGTGATTTGGCATGACCGAGGCTGACCTGTGGCTTGTGGGAAACACAGCC 440
DB 121 LeuLysAlaValIleGlyMetThrAlaGlyAlaThrGlyAlaPheValGlyThrProAla 140
QY 441 GAAGTGGCTCTTATCCGATGATGCGCATGCGGCTTCAGCTGACACGAGCGCTGGC 500
DB 141 GluValAlaLeuLeuLeuThrAlaAspGlyArgLeuProAlaAspGlnArgGly 160
QY 501 TACAAAATGTGTTTAAACGCTGATTCGAATACCCGGAGAGAGGGTGTCTTCACACTG 560
DB 161 TyrLysAsnValPheAsnAlaLeuIleArgIleThrArgGlnGlyValLeuThrLeu 180
QY 561 TGGCGGGGCTGATCCCTACATGAGCTGGGCGGCTGCTGATGCTGCCAGCTGGC 620
DB 181 TrpArgGlyCysIleProThrMetAlaArgAlaValValAsnAlaAlaGlnLeuAla 200
QY 621 TCCCTATCCCAATCCCAAGAGTCTTACTGAACTCAGGCTACTTCTCTGCAACATCTG 680
DB 201 SerTyrSerGlnSerIleArgGlnPheLeuLeuAspSerGlyTyrPheSerArgPheLeu 220
QY 681 TGGCACTTCTGTGGCAGCATGATGACGGCTTGTGCAACACTGCTGCTCATGCTGTG 740
DB 221 CysHisPheCysAlaSerMetIleSerGlyLeuValIleThrThrAlaIleSerMetProVal 240
QY 741 GACATGGCCAAAGCCGAATCCGAACATGCGGATGATGATGATGAGGAACCGGAATCAAG 800
DB 241 AspIleAlaLysThrArgIleGlnAsnMetArgMetIleAspGlyLysProGlnTyrLys 260
QY 801 AACGGGCTGGACGCTGCTTCAAGAGTTGTCGCTACGAGGGCTTCTTCAAGCTGTGAAG 860
DB 261 AsnGlyLeuAspValLeuPheLysValValArgTyrGlnGlyPhePheSerLeuTrpLys 280
QY 861 GGCTTACGCGCGTACTATGCGCGCTGGGCGCCCAACCGTCTCTCATCTTCTTG 920
DB 281 GlyPheThrProTyrTyrAlaArgLeuGlyProHisThrValLeuThrPheIlePheLeu 300
QY 921 GAGCAGATGAACAAAGGCTTCAAGCGTCTTCTTCTCATGAGC 962
DB 301 GlnGlnMetAsnLysAlaTyrLysArgLeuPheLeuSerGly 314

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RESULT 2

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OSRFJ5_PONPY PRELIMINARY; PRT; 314 AA.
AC OSRFJ5;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DE Hypothetical protein DKFZp468G0316.
GN Name=DKFZp468G0316.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;

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OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Heart;
RG The German cDNA Consortium;
RA Bahr A., Leuber J., Mewes H.W., Weil B., Amid C., Oanger A., Fobo G.,
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR857161; CAH89462.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO; GO:0005488; P:binding; IEA.
DR GO; GO:0005215; P:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002113; Aden_transloc.
DR InterPro; IPR001993; Mitoch_carrier.
DR Pfam; PF00153; Mitc_car; 3.
DR PRINTS; PR00927; ADPTRNSLCASE.
DR PROSITE; PS50920; SOLCAR; 3.
KW Hypothetical protein; Transmembrane; Transport.
SQ SEQUENCE 314 AA; 34047 MW; 9BCC4C637F8130FA CRC64;

Alignment Scores:
Pred. No.: 1,68e-106 Length: 314
Score: 1600.00 Matches: 313
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 99.7% Mismatches: 0
Query Match: 73.4% Indels: 0
DB: 2 Gaps: 0

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DB 1 MetAlaAlaThrAlaSerHisAlaGlyAlaGlyGlyMetAspGlyLysProArgThrSerPro 20
QY 81 AAGTCCGTCAGAGTTCCTGTTTGGGGGCTGGCCGGATGGAGCTACAGTTTTCACG 140
DB 21 LysSerValLysPheLeuPheGlyGlyLeuAlaGlyMetGlyAlaThrValPheValGln 40
QY 21 CCCCTGAGCTGGTGAAGAAACCGGATGCACTTGAAGCGGGAGAGGGCCAAAGACTCGAAG 200
DB 41 ProLeuAspLeuValLysAsnArgMetGlnLeuSerGlyGlnGlyAlaThrValArgGln 60
QY 141 GAGTGGGCTGTGATTTGGCATGACCGAGGCTGACCTGTGGCTTGTGGGAAACACAGCC 440
DB 121 LeuLysAlaValIleGlyMetThrAlaGlyAlaThrGlyAlaPheValGlyThrProAla 140
QY 441 GAAGTGGCTCTTATCCGATGATGCGCATGCGGCTTCAGCTGACACGAGCGCGTGGC 500
DB 141 GluValAlaLeuLeuLeuThrAlaAspGlyArgLeuProAlaAspGlnArgGly 160
QY 501 TACAAAATGTGTTTAAACGCTGATTCGAATACCCGGAGAGAGGGTGTCTTCACACTG 560
DB 161 TyrLysAsnValPheAsnAlaLeuIleArgIleThrArgGlnGlyValLeuThrLeu 180
QY 561 TGGCGGGGCTGATCCCTTACATGAGCTGGGCGGCTGCTGATGCTGCCAGCTGGC 620
DB 181 TrpArgGlyCysIleProThrMetAlaArgAlaValValAsnAlaAlaGlnLeuAla 200

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QY	81	AAAGTCCGTCAGAGTTCTGTGTTGGGGGGCTCGGCGGAGATGGAGGCTACAGTTTGTGTCCAG	140
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QY	141	CCCCGTGACCTGTGTGAAGAACCGGATGTGACGTTGAGCGGGGGAAGGGGCCAAGACTCGAGAG	200
Db	41	PROLEUAEPLEUVALVYSAENHARGMETGLNEUSERGYGLUGLYALALYVETTRHARGJLN	60
QY	201	TACAAAACACAGCTTCATGCCCTCACCGATATCTTGAAAGGCAGAAAGCCTGAGGGGCATT	260
Db	61	TYRYSRTIRSRPHEHISALALEUTHSRILEUYSALAGIUGLYLEUARGLYLE	80
QY	261	TACACTGGGCTGTGGGCTGGGCTGGTGGTCAAGGCACCTACACACACTACCCGCTTGGC	320
Db	81	TYRTHRGLYLEUSERALAGLYLEULEUARGLNALATHRYRTHRTHRHARGLEUGLY	100
QY	321	ATCTATACCGTGCTGTGTTTGAAGCGCTGACTGGAGCTGATGGTACTCCCCCTGAGCTTTCTG	380
Db	101	ILETRYRTHRALLEUPHEGLIARGLEUTHRGILYALAEPSGLYTHRPROPSGLYPHELEU	120
QY	381	CTGAAGCGCTGATGATTGGCATGACCGCAGAGTGCACCTGGTGCCTTTGGGGAACACAGCC	440
Db	121	LEUYSALALVALIILEGLYMETRHALAGLYALATHRGYALAEVALGLYTHRPROLA	140
QY	441	GAAGTGGCTCTTATCCGCGATGACTGCGGATGGCGGCGGCTTCCAGCTGACACAGCGCGTGGC	500
Db	141	GLIIVALALALEUILLIARGMETRHALAEPSGLYARGLEUPROILAEPGLIARGGLY	160
QY	501	TACAAAAATGTGTTTAAAGCCCTGATTTGGATATCACCCGGGAAGAGGGTGTCTTACACTG	560
Db	161	TYRYSAAENVALPHEAENVALALEUILLIETHRARGIUGIUGLYVALLEUTHRLEU	180
QY	561	TGGCGGGGCTCATCTCCATCCATGAGCTCGGGCCGTGTCGTCAATGCTGCCACCTGCC	620
Db	181	TRPARGIYCYBIIERPROTHMETALARGHIALVALVALAENALALAGIENUALA	200
QY	621	TCCTAATCTCCCAATCCAGACAGTTCTTACTGGACTCAGGCTACTTCTGTGACACATCTGTG	680
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QY	681	TGCCACTCTGTGCGCAGCATGATACGCGGTCTMTGCAACATGCTGCTCCATGCTGTG	740
Db	221	CYSHSPHECYBALASERMETIILESERGLYEUVALTHRTIRHIALASERMETPROVAL	240
QY	741	GACATTGCCAAGACCCGGAATCCAGAACATGCGAGTATGATGGGAACCGGAAATACAG	800
Db	241	ASPIILEALALYSTHARGIIIEGLINAMETARGMETIIAEPSGLYLYSPROGLIUTRYLYS	260
QY	801	AACGGGCTGAGAGTGTCTTAAAGTTGTCCGCTACGAGGGCTTCTCAGCTGTGGAAG	860
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QY	861	GGCTTCACGCGGTACTATGCGCGCTGGGCGCCCAACACGTCCTACCTTCATCTTCTTG	920
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R:Iacobazzi, V.; Palmieri, F.; Runswick, M.J.; Walker, J.E.
DNA Seq. 3, 79-88, 1992
A:Title: Sequences of the human and bovine genes for the mitochondrial 2-oxoglutarate carrier
A:Reference number: A56650; MUID:93091249; PMID:1457618
A:Accession: B56650
A:Status: preliminary
A:Molecule type: DNA
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A:Note: sequence extracted from NCBI backbone (NCIN:120086, NCIP:120087)
R:Iacobazzi, F.; Zaza, V.; Capobianco, L.; Iacobazzi, V.; Mazzeo, M.; Palmieri, F.
Biochim. Biophys. Acta 1292, 281-288, 1996
A:Title: The formation of a disulfide cross-link between the two subunits demonstrates th
A:Reference number: S65731; MUID:96176856; PMID:8597574
A:Accession: S65731
A:Status: preliminary
A:Molecule type: protein
A:Residues: 148-160 <BI>
A:Cross-references: UNIPARC:UPI0000177A24
R:Iacobazzi, F.; Capobianco, L.; Brandolin, G.; Palmieri, F.
Biochemistry 33, 3705-3713, 1994
A:Title: Transmembrane topography of the mitochondrial oxoglutarate carrier assessed by E
A:Reference number: A54249; MUID:94190892; PMID:8142370
A:Accession: A54249
A:Status: preliminary
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A:Cross-references: UNIPARC:UPI0000177A25, UNIPARC:UPI0000177A26, UNIPARC:UPI0000177A27,
R:Iacobazzi, F.; Capobianco, L.; Mazzeo, M.; Palmieri, F.
FEBS Lett. 392, 54-58, 1996
A:Title: The mitochondrial oxoglutarate carrier protein contains a disulfide bridge betwe
A:Reference number: S71377; MUID:96354876; PMID:8769314
A:Accession: S71377
A:Molecule type: protein
A:Residues: 148-160;189-200 <BI>
A:Cross-references: UNIPARC:UPI0000177A24; UNIPARC:UPI0000177A2C
A:Experimental source: heart
C:Genetics:
A:Introns: 32/2; 83/2; 246/2; 263/3
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C:Keywords: duplication; mitochondrion; transmembrane protein
F:18-109/Domain: ADP,ATP carrier protein repeat homology <ACPI>
F:116-209/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F:216-307/Domain: ADP,ATP carrier protein repeat homology <ACP3>
F:221-224/Disulfide bonds: #status experimental

Alignment Scores:
Pred. No.: 5.27e-109 Length: 314
Score: 1549.00 Matches: 303
Percent Similarity: 97.1% Conservative: 2
Best Local Similarity: 96.5% Mismatches: 9
Query Match: 71.0% Indels: 0
DB: 2 Gaps: 0

US-09-888-264-1 (1-1123) x A36305 (1-314)

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DB 1 MetalaalathAlaSerProGlyAlaSerGlyMetAspGlyLysProAlyThrSerPro 20
QY 81 AAGTCGCGAAGTTCTCTGTTGGGGGCGTGGCGGAGATGGAGACTCAGTTTGTCCAG 140
DB 21 LysSerValLysPheLeuPheGlyGlyLeuAlaGlyMetGlyAlaThrValPheValGln 40
QY 141 CCCCTGACCTGGTGAAGAACCGATGACATTGACGGGGAGAGGGGCAAGACTCGAGAG 200
DB 41 ProLeuAapLeuValLysAsnArgMetGlnLeuSerGlyGluGlyAlaLysThrArgGlu 60
QY 201 TACAAACACAGTTCCTCATGCCCTCACCAAGTATCTCGAAGCAGAAAGCCCTGAGGGGCAATT 260
DB 61 TyLysThrSerPheIleAlaLeuIleSerIleLeuArgAlaGluGlyLeuAlaGlyIle 80

PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
 PI Warnock DE;
 XX
 DR MPI; 2003-845369/78.
 XX
 PT Identifying a mitochondrial target for drug screening assays and for
 PT treating diseases associated with altered mitochondrial function,
 PT comprises detecting a modified polypeptide in a sample and correlating
 PT with the disease.
 XX
 PS Claim 1; SEQ ID NO 498; 180bp; English.
 XX
 CC This invention relates to novel mitochondrial targets that can be used
 CC for therapeutic intervention in treating a disease associated with
 CC altered mitochondrial function. Specifically, it refers to a method for
 CC identifying proteins of the human heart mitochondrial proteome that are
 CC useful for drug screening assays, as well as therapeutic targets. The
 CC present invention describes a method for identifying such proteins that
 CC can be used in the treatment of various diseases associated with altered
 CC mitochondrial function including diabetes mellitus, Huntington's disease,
 CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
 CC encephalopathy, lactic acidosis and stroke (MELAS), myoclonic epilepsy
 CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
 CC compositions have neuroprotective, nootropic, antidiabetic,
 CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
 CC cytostatic activities. This polypeptide sequence is a human heart
 CC mitochondrial protein of the invention.
 XX
 SQ Sequence 314 AA;

Alignment Scores:
 Pred. No.: 4,93e-133 Length: 314
 Score: 1604.00 Matches: 314
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 73.5% Indels: 0
 DB: 7 Gaps: 0

US-09-888-264-1 (1-1123) x ABD68692 (1-314)

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 QY 81 AAGTCGCGTGAAGTTCCTGTTGGGGGCGCGGATGAGGACTCAAGTTTTCGCG 140
 DB 21 LysSerValLysPheLeuPheGlyGlyLeuAlaGlyMetGlyAlaThrValPheValGln 40
 QY 141 CCCCTGAGCTGGTGAAGAACCGGATGAGTTCAGCGGAGGCGCAAGACTCCAGAG 200
 DB 41 ProLeuAspLeuValLysAsnArgMetGlnLeuSerGlyGlnLysAlaLysThrArgGln 60
 QY 201 TACAAAACGAGCTTCATGCGCTTACCAAGTATCTTGAAGGAGAGGCTTGAAGGCGCAT 260
 DB 61 TyrLysThrSerPheHisAlaLeuThrSerIleLeuLysAlaGlnLysLeuArgGlyIle 80
 QY 261 TACAGCGGCTGTCGCGTGCCTGCTGCTGACGACCACTACACCACTACCGCCTTGGC 320
 DB 81 TyrThrGlyLeuSerIleGlyLeuLeuArgGlnAlaThrLysThrThrArgLysLeuGly 100
 QY 321 ATCTATACGCTGCTGTTGAGCGCTGATCGGAGGCTGATGTAATCCCTCGGCTTTCG 380
 DB 101 IleTyrThrValLeuPheGlnArgLeuThrGlyAlaIleAspGlyThrProProGlyPheLeu 120
 QY 381 CTGAAGCGCTGTGATGGCATGACCGAGGTGCACCTGTGCTTGTGGAGACACGAGCC 440
 DB 121 LeuLysAlaValIleGlyMetThrAlaGlyAlaThrGlyAlaPheValGlyThrProAla 140
 QY 441 GAAGTGCTTTATCCGATGACTGCCGATGCGCGGCTTCCAGCTGACCGCGCGTGGC 500
 DB 141 GluValAlaLeuIleArgMetThrAlaAspGlyArgLeuProAlaAspGlnArgGly 160
 QY 501 TACAAAAGTGTGTTAAGCGCTGATTCGAATCACCGCGGAGAAAGGCTGTCTCACACTG 560

DB 161 TyrLysAsnValPheAsnAlaLeuIleArgIleThrArgGlnGlnGlyValLeuThrLeu 180
 QY 561 TGGCGGCGCTGATCCCTACATGAGTGGGCGTGTGCTCAATGCTGCCAGCTGCGC 620
 DB 181 TrpArgGlyCysIleProThrMetAlaArgAlaValValAsnAlaIleGlnLeuAla 200
 QY 621 TCTTACTCCCAATCCAGAGCTTCTTACTGACTGAGCTGAGCTTCTTTCAGACATCTG 680
 DB 201 SerTyrSerGlnSerIleGlnPheLeuAspSerGlyTyrPheSerAspIleLeu 220
 QY 681 TGGCACTTGTGGCCAGCATGATCAGCGGCTTTGTGACACACTGCTGCTCCATGCTGTG 740
 DB 221 CysHisPheCysAlaSerIleSerGlyLeuValThrThAlaIleSerMetProVal 240
 QY 741 GACATTGCCAAGACCCGATCCAGAACATGCGGATGATGATGAGGAGCGGAATCAAG 800
 DB 241 AspIleAlaLysThrArgIleGlnAsnMetArgMetIleAspGlyLysProGlnTyrLys 260
 QY 801 AACGGGCTGAGCGTGTTCAAAGTTTCGCTACGAGGCTTCTTTCAGCTGTGGAAG 860
 DB 261 AsnGlyLeuAspValLeuPheLysValAlaArgTyrGlnGlyPhePheSerLeuTyrLys 280
 QY 861 GCGTTACGCGCTACTATGCTCCGCTGGGCGCCGACACCGTCTCACTTATCTTCTTG 920
 DB 281 GlyPheThrProTyrTyrAlaArgLeuGlyProHisThrValLeuThrPheIlePheLeu 300
 QY 921 GAGCAGATGACAAAGCGCTTCACAGCGTCTCTCCCTCAGTGGC 962
 DB 301 GluGlnMetAsnLysAlaTyrLysArgLeuPheLeuSerGly 314

RESULT 2
 ID ABG75060 standard; protein; 314 AA.
 AC ABG75060;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Human solute carrier family 25 member 11 protein.
 XX
 KW Energy homeostasis; mouse; metabolism; triglyceride; metabolic disease;
 KW gene therapy; anorectic; immunomodulator; antidiabetic; hypotensive;
 KW cardiac; osteopathic; antilipemic.
 XX
 OS Homo sapiens.
 PN WO2003075945-A2.
 XX
 PD 18-SEP-2003.
 XX
 PF 14-MAR-2003; 2003WO-BP002714.
 XX
 PR 14-MAR-2002; 2002EP-00005882.
 PR 15-MAR-2002; 2002EP-00006012.
 PR 20-MAR-2002; 2002EP-00006271.
 PR 25-MAR-2002; 2002EP-00006810.
 XX
 PA (DEVE-) DEVELOPEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
 XX
 PI Eulenberger K, Steuernagel A, Haeder T, Broemner G;
 XX
 DR MPI; 2003-748334/70.
 DR N-PSDB; ACH00820.
 XX
 PT New pharmaceutical composition comprising a nucleic acid molecule
 PT encoding proteins regulating the energy homeostasis and metabolism of
 PT triglycerides useful for detecting or preventing metabolic diseases, e.g.
 PT obesity.
 XX
 PS Claim 3; Fig 11C; 140bp; English.
 XX
 CC The present invention relates to pharmaceutical compositions comprising


```
/ Sequence 57090, Application US/10750623
/ Publication No. US20050287531A1
/ GENERAL INFORMATION:
/ APPLICANT: MMT GENOMICS, INC.
/ APPLICANT: DENISE, Sue K.
/ APPLICANT: KERR, Richard
/ APPLICANT: ROSENFELD, David
/ APPLICANT: HOLM, Tom
/ APPLICANT: BATES, Stephen
/ APPLICANT: PANTIN, Dennis
/ TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
/ FILE REFERENCE: M11100-1
/ CURRENT APPLICATION NUMBER: US/10/750,623
/ CURRENT FILING DATE: 2003-12-31
/ PRIOR APPLICATION NUMBER: US 60/437,482
/ PRIOR FILING DATE: 2002-12-31
/ NUMBER OF SEQ ID NOS: 64922
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 57090
/ LENGTH: 987
/ TYPE: DNA
/ ORGANISM: Bovine 19866880933603
US-10-750-623-57090

Query Match 12.1%; Score 136.2; DB 7; Length 987;
Best Local Similarity 89.1%; Pred. No. 1.9e-28;
Matches 147; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 112 CCGGATGGAGCTACAGTTTGTCCAGCCCTGAGCTGTGAGAAACCGGATGCAGT 171
DB 177 CCGGATGGAGCTACAGTTTGTGCGAGCCCTTGAGCTGTGAGAAACCGGATGCAGC 118
QY 172 TGAGCGGGGAAAGGCGCAAGACTGAGAGTACAAAACAGCTTCATGCCCTCAGCAGTA 231
DB 117 TGAGTGGGAAAGAGCCAGACACAGAGTACAAAACAGCTTCATGCCCTCAGCAGCA 58
QY 232 TCCTGAAAGCAGAGGCTGAGGGGCAATTACACTGCGCTGTGCG 276
DB 57 TCCTGAGGGGAGAAAGGCTTATGGGCAATTACACCGGCTACTGGG 13

RESULT 3
US-11-136-527-3307
/ Sequence 3307, Application US/11136527
/ Publication No. US20050287570A1
/ GENERAL INFORMATION:
/ APPLICANT: Wyeth
/ APPLICANT: Mounes, William M
/ TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
/ FILE REFERENCE: 031896-041000 (AM101086)
/ CURRENT APPLICATION NUMBER: US/11/136,527
/ CURRENT FILING DATE: 2005-05-25
/ PRIOR APPLICATION NUMBER: US 60/574,294
/ PRIOR FILING DATE: 2005-05-26
/ NUMBER OF SEQ ID NOS: 362830
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 3307
/ LENGTH: 1339
/ TYPE: DNA
/ ORGANISM: Rattus norvegicus
US-11-136-527-3307

Query Match 10.7%; Score 120; DB 8; Length 1339;
Best Local Similarity 48.1%; Pred. No. 8.1e-24;
Matches 416; Conservative 0; Mismatches 430; Indels 18; Gaps 2;
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QY 201 TACAAAACAGCTTCCATGCCCCCTACACAGTATCTCTGAAGGAGGAGGCTGAGGGGCAATT 260
DB 298 TACCGGAGGCTGCTCGGTACCATCTGACTATGTGTGCGACAGAGGGTCCCGGACCC 357
QY 261 TACACTGGGCTGTGCGCTGCGCTGCTGCGTCAAGGCCACTACACACTACCCGCTTGGC 320
DB 358 TACAGCGGCTGGTGTGCTGGCTGCGCTGCGCTGCGTCAAGATGATTTTGCCTCAATTGGA 417
QY 321 ATCTATACCGTGTCTTTAGCGCCCTGACTGGGGCTGATGTACTCCCTGGCTTTCG 380
DB 418 CTCTACGACTCTGTCAAGCAGTTTCAACCCCCCAAGAAAGGACCACTCCAGCGTCC 477
QY 381 CTGAAGCTGTGATTTGGCATGACCCGAGGTGCACTGTGCTTTGTGGAAACACAGCC 440
DB 478 ATCAGATTTCTGGCAGCGCTGACACACGGAAGCATGTGATGACTGTGTCAACCCAG 537
QY 441 GAAGTGCTCTTATTCGCATGACTGCGATGGCGGCTTCCAGCTGACCAAGCGCGTGGC 500
DB 538 GATGTGTGAAGTCCGATTTCAAGCCATGATACGCTGGAACTGGAGGCGAGAGAAA 597
QY 501 TACAAAATGTGTTTACCGCCCTGATTCGAATCACCCGGGAAAGAGGTGTCTCAACATG 560
DB 598 TACAGAGGACTATGATGATGCTTACAGAACCATGCTCAAGGAAAGAGGAGGAGGACTG 657
QY 561 TGGCGGGCTGCTATCCCTACATGAGCTCGGGCGGTGCTGATCAATGCTGCCAGCTCGCC 620
DB 658 TGGAAAAGGACTTGGCGCCCACTACACAAAGAACCATTTGTCAATTGTGTGATGATG 717
QY 621 TCCTACTCCCAATCCAAAGAGTTCTTACTGAGCTCAGGCTACTTCTGACCAATCTTG 680
DB 718 ACTATGATCATCATCAAGAGAAAGTGTGACTGCTGACTGCTGCTGCTGCTGCTGCTGCT 777
QY 681 TGCATTTCTGTGCGCAGCATGATCAGCGTCTTGTACCACTGCTGCTGCTGCTGCTG 740
DB 778 TGTCACTTGTGTCTGTGCTTGTGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 837
QY 741 GACATTTGCAAGACCCGAATCCAGAACTGCGATGATTTGATGGAAGCCGGAATTCAG 800
DB 838 GATGTGTAAAGACCCGATAC-----ATBAAGCTCCCCCAAGGAGTACCGA 885
QY 801 AACGGGCTGAGCTGTGCTTCAAAAGTGTCCGCTACGAGGGCTTCTTCAGCTGTGGAAG 860
DB 886 AGCCCCCTACACTGTATGTGTGAGATGTGTGCGCCAGAGAGGCCCAAGCCTTCTACAA 945
QY 861 GGTTCAGCCGTATCTATGCCCCCTGCGGCCCAACCGTCTCATCTTCTTCTG 920
DB 946 GATTCATGCTCTCTCTTGTGCTGTGGATCTGTGAACGTATGATGTTGTAACTTAC 1005
QY 921 GAGCAGATGACAGGCTTACAG 944
DB 1006 GAGCAGCTGAAGCGGCTTGATG 1029

RESULT 4
US-11-010-239-108
/ Sequence 108, Application US/11010239
/ Publication No. US20060015970A1
/ GENERAL INFORMATION:
/ APPLICANT: Roger PENNELL
/ APPLICANT: Jack OKAMURO
/ APPLICANT: Richard SCHNEEBERGER
/ APPLICANT: Ylwen FANG
/ APPLICANT: Shing KWOK
/ APPLICANT: Diane JOFURU
/ APPLICANT: Edward A. KIEGLE
/ APPLICANT: Jonathan DONSON
/ APPLICANT: Nestor APIYA
/ TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY USEFUL FOR
/ FILE REFERENCE: 2750-1585P02
/ CURRENT APPLICATION NUMBER: US/11/010,239
/ CURRENT FILING DATE: 2004-12-09
```


Db	266	GGCGGTGGCTACAAAAAATGTGTTTAAAGCGCCGATTCGAAATCACCCGGGAAGAAGGGTGTCTC	207
Qy	552	CTCACACTGTGTGGCGGGGCTGCATTCCTTACCAATAGCTGGGCGGTGTCTGTCAATGCTGCC	611
Db	206	CTCAACACTGTGGCGGGGCTGCATTCCTTACCAATAGCTGGGCGGTGTCTGTCAATGCTGCC	147
Qy	612	CAGCTCGGCTCCTTACTCCCAATCCAAAGCAGTCTTACTGGA-CTCAGGGCTACTCTCTGA	670
Db	146	CAGCTCGGCTCCTTACTCCCAATCCAAAGCAGTCTTACTGGAATCCCAAGGCTACTCTCTGA	87
Qy	671	CAACAATCTGTGCCAATTCCTGTGCAGCAGATGATCAGCGGTCTTGTACCACTGCTGCTTC	730
Db	86	CAACAATCTGTGTGCCAATTCCTGTGCAGCAGATGATCAGCGGTCTTGTACCACTGCTGCTTC	27
Qy	731	CATGCTGTGACATTTGCCAAGACC	756
Db	26	CATGCTGTGACATTTGCCAAGACC	1

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RESULT 2
US-09-949-016-15809/c
; Sequence 15809, Application US/09949016
; Patent No. 6812319
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 15809
; LENGTH: 11073
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15809

Query Match      24.0%; Score 269.4; DB 3; Length 11073;
Best Local Similarity 81.1%; Pred. No. 4e-60;
Matches 364; Conservative 0; Mismatches 1; Indels 84; Gaps 1;

Dy      112  CCGGATGGAGACTACAGTTTGTTCACAGCCCTGTGACCTCTGGAGAAACCGGATGCAGT 171
Db      3062  CCAGATGGAGACTACAGTTTGTTCACAGCCCTGTGAGAAACCGGATGCAGT 3003

Dy      172  TGAGGGGGAAAGGGGCCAAGACTCGAGAGTACAAACCAAGCTTCAGTGCCTCAGCAGTA 231
Db      3002  TGAGGGGGAAAGGGGCCAAGACTCGAGAGTACAAACCAAGCTTCAGTGCCTCAGCAGTA 2943

Dy      232  TCCTGAAGGCAGAAAGGCTGAGGGGCAATTACATG----- 267
Db      2942  TCCTGAAGGCAGAAAGGCTGAGGGGCAATTACATGCGATTGGGGCTTCAGGATGGAGG 2883

Dy      268  ----- 267
Db      2882  GTAGACTGGGTTGGCAAGCTTAGACCTTGGCCTGATATGCTGAGACCCCTGCTCTCA 2823

Dy      268  GGGCTGCGGCTGGCGCTGCGGTCAGGGCCACACTACACGACTACCGGCTTTGGCATCATTA 327
Db      2822  GGGCTGCGGCTGGCGCTGCGGTCAGGGCCACACTACACGACTACCGGCTTTGGCATCATTA 2763

Dy      328  CCGTGTCTTTTGGAGCGCTGACTGTGGGCTGATGGTACTCCCTGTGCTTTCTGTGAAG 387
Db      2762  CCGTGTCTTTTGGAGCGCTGACTGTGGGCTGATGGTACTCCCTGTGCTTTCTGTGAAG 2703

Dy      388  CTGTGATTGGCATGACCGGAGTGCCACTGTGTGCTTTGTGGAGACACGACCGAAGTGG 447

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Accession	Sequence	Length
D6	CTGTGATTGGCATACCCGCGAGGTGCACTGATGCTCTTTGTGGAAACACGACCGGAGTGG	2702
Oy	CTCTTATCCGCATGACTGACCGCATGGCCGG	448
D6	CTCTTATCCGCATGACTGACCGCATGGCCGG	2642

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RESULT 3
US-09-620-312D-874
; Sequence 874; Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yuning
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinphast
; APPLICANT: Drmanac, Radote T.
; TITLE OF INVENTION: No. 656962e1 Nucleic Acids and
; FILE REFERENCE: Polypeptides
; CURRENT APPLICATION NUMBER: US/09/620,312D
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pf_fl_genes Version 1.0
; SEQ ID NO 874
; LENGTH: 2003
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (194)..(1057)
US-09-620-312D-874

Query Match          11.5%; Score 128.6; DB 3; Length 2003;
Best Local Similarity 52.8%; Pred. No. 1.3e-23;
Matches 278; Conservative 0; Mismatches 249; Indels 0; Gaps 0;

QY      241 CAGAAAGCCTGAGGGGCAATTACACTGAGCTGTGCGCTGCGCTGCTGCTGAGGCACCT 300
DB      354 CCGAGCGGATCTGTGCACTTACAGCGGCTGAGCGCTGCTGCTGCTGCTGCAAGATGACCT 413

QY      301 ACACCACTACCCGCGCTTGGCATCTATACCGGCTGTTGAGCGGCTGACTGAGGCTATG 360
DB      414 ACTCCCTGACTCGGCTTGCCATCTACGAGACTGTGCGGAGCGGCTGCTGCTGCAAGGCGACC 473

QY      361 GTACTCCCTCGGCTTTCGTGCTGAAGCTGTGATTTGCGATGACCGCAGGTGCCACTGTGTG 420
DB      474 AGGGGCTCTTCCCTTCCACGAGAAAGTGTGCTGGGCTCCGTACAGCGGTTTGAAGTGGAG 533

QY      421 CTTTGTGGGAACCAACGCGGAGTGTCTTATCCGATGACTGCGATGAGCCGCGCTTC 480
DB      534 GCTTCGTGGGAGACCCCGCAGACTTGTGCAACGTGAGATGACAGAACGACGTGAAGCTGC 593

QY      481 CAGCTGACCAAGCGCGGTGCTACCAAAAATGTGTTTAAGCCCTGATTCGAATCAACCCGCG 540
DB      594 CCGAGGCTACCGGCGCAACTTACGCGCCATGCGTGAATGAGGCTGTATCCGCTAGCTGTG 653

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 2, 2006, 00:52:24 ; Search time 4960.27 Seconds
(without alignments)
10592.541 Million cell updates/sec

Title: US-09-888-264-1
Perfect score: 1123
Sequence: 1 ccgagggccatgagtgagcgc.....ctcatgagactcaataa 1123

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST.*
1: gb_esc1.*
2: gb_esc2.*
3: gb_esc3.*
4: gb_hic.*
5: gb_esc4.*
6: gb_esc5.*
7: gb_esc6.*
8: gb_esc7.*
9: gb_gsa1.*
10: gb_gsa2.*
11: gb_gsa3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	968.6	86.3	1369	4	CR590793 full-leng
2	968.6	86.3	1386	4	CR606322 full-leng
3	968.6	86.3	1429	4	CR620583 full-leng
4	968.6	86.3	1467	4	CR603391 full-leng
5	968.6	86.3	1477	4	CR617034 full-leng
6	968.6	86.3	1479	4	CR595953 full-leng
7	968.6	86.3	1488	4	CR591200 full-leng
8	968.6	86.3	1515	4	CR617848 full-leng
9	968.6	86.3	1529	4	CR598517 full-leng
10	968.6	86.3	1532	4	CR609603 full-leng
11	968.6	85.9	1051	4	CR616117 full-leng
12	968.6	85.9	1369	4	CR590943 full-leng
13	968.6	85.9	1345	4	CR615026 full-leng
14	968.6	84.8	1432	4	CR857161 Pongo pvs
15	947.6	84.4	1147	5	CR613107 full-leng
16	944.6	84.1	1302	4	CR613107 full-leng
17	944.6	84.1	1358	4	CR625556 full-leng
18	942.6	83.9	1354	4	CR613184 full-leng
19	941.8	83.9	945	10	AY415734 Homo sapi
20	941.4	83.8	1058	5	AX333400 BX333400
21	915.2	81.5	1159	5	AL529560 AL529560
22	908.6	80.9	1090	5	BX363653 BX363653

23	908	80.9	1125	1	AL519985	AL519985
24	902.2	80.3	1174	5	BX424850	BX424850
25	898.6	80.0	1117	5	BX381492	BX381492
26	896	79.8	1087	5	BX463231	BX463231
27	890.8	79.3	1043	5	BX400267	BX400267
28	889.2	79.2	1039	1	AL580443	AL580443
29	888.8	79.1	1165	1	AL547659	AL547659
30	885.8	78.9	1017	5	BX397004	BX397004
31	874.4	77.9	1121	1	AL530824	AL530824
32	865.6	77.1	899	5	BX393630	BX393630
33	857.6	76.4	1271	4	CR600572	CR600572
34	852	75.9	871	1	AL520894	AL520894
35	833.2	74.2	899	5	BX354584	BX354584
36	831	74.0	1441	5	BX394275	BX394275
37	828	73.7	873	2	BG764317	BG764317
38	816.2	72.7	1464	4	AK009824	AK009824
39	816.2	72.7	1634	4	AK009487	AK009487
40	813.2	72.4	1061	3	BM921558	BM921558
41	813	72.4	850	10	AY415735	AY415735
42	812.4	72.3	1003	3	BM924580	BM924580
43	812	72.3	1055	3	BT577743	BT577743
44	810.6	72.2	1149	5	BX447797	BX447797
45	809.8	72.1	813	8	DR763694	DR763694

ALIGNMENTS

RESULT 1
CR590793 1369 bp mRNA linear HTC 21-JUL-2004
LOCUS
DEFINITION
Full-length cDNA clone CS0DC025YC08 of Neuroblastoma Cot
25-normalized of Homo sapiens (human).

ACCESSION
CR590793
VERSION
CR590793.1 GI:50471600
KEYWORDS
HTC; CNS/IT CDNA.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
Eumetazoa; Metazoa; Euteleostomi; Euteleostomi;
Mammalia; Euteleostomi; Euteleostomi; Euteleostomi;
Homidae; Homo.
1 (bases 1 to 1369)

REFERENCE
AUTHORS
TITLE
JOURNAL
REMARK
Li, W.B., Gruber, C., Jesses, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Feng Liang Email: fliang@life.rockefeller.edu
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Parade Avenue
2 (bases 1 to 1369)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with NotI and cloned
into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
Location/Qualifiers
1. 1369
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DC025YC08"
/issue_type="Neuroblastoma Cot 25-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN
Query Match 86.3%; Score 968.6; DB 4; Length 1369;
Best Local Similarity 99.1%; Pred. No. 1e-240;
Matches 974; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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QY 1 CCGAGGGCCATTGATGCGATGCGGCGACGCGGATGCGCGGCGGCGGATGAGCG 60
DB 8 CCGAGGGCCATTGATGCGATGCGCGGCGACGCGGATGCGCGGCGGCGGATGAGCG 67
QY 61 GGAAGCCCGGATCTCCCTTAAGTCCGTCAAGTTCTGTTGGGGGCTGCGCGGATG 120
DB 68 GGAAGCCCGGATCTCCCTTAAGTCCGTCAAGTTCTGTTGGGGGCTGCGCGGATG 127
QY 121 GAGCTACAGTTTGTTCAGCCCGCTGAGCCTGCTGAGAAACCGGATGAGCGGG 180
DB 128 GAGCTACAGTTTGTTCAGCCCGCTGAGCCTGCTGAGAAACCGGATGAGCGGG 187
QY 181 AAGGGCCAAAGACTCGAAGTACAAAACAGCTTCCATGCGCTCACCAGTATCTGAAG 240
DB 188 AAGGGCCAAAGACTCGAAGTACAAAACAGCTTCCATGCGCTCACCAGTATCTGAAG 247
QY 241 CAGAAAGCCCTGAGAGGCGATTATACATGAGCTGCTGCGCTGCGCTGCGGCGG 300
DB 248 CAGAAAGCCCTGAGAGGCGATTATACATGAGCTGCTGCGCTGCGCTGCGGCGG 307
QY 301 ACACCACTACCCGCTTGGCATCTATACCGTGTGCTTTGAGGCGCTGAGCTGGGCGT 360
DB 308 ACACCACTACCCGCTTGGCATCTATACCGTGTGCTTTGAGGCGCTGAGCTGGGCGT 367
QY 361 GTAATCCCTGCTTCTGCTGAGGCTGCTGATGAGGATGAGCGAGTGCACCTGATG 420
DB 368 GTAATCCCTGCTTCTGCTGAGGCTGCTGATGAGGATGAGCGAGTGCACCTGATG 427
QY 421 CTTTGTGGGAACACACCGGAAAGTGCTTTATCCGATGACTGCCGATGCGCGCTTC 480
DB 428 CTTTGTGGGAACACACCGGAAAGTGCTTTATCCGATGACTGCCGATGCGCGCTTC 487
QY 481 CAGCTACCAAGGCGCGGAGTACAAAAGTGTGTTAAAGCGCTGATTCGAATCACCG 540
DB 488 CAGCTACCAAGGCGCGGAGTACAAAAGTGTGTTAAAGCGCTGATTCGAATCACCG 547
QY 541 AAGAGGGGTCTCTACACTGTGCGGCGCTGATCCCTACCAAGGCTGCGCGCTGCTG 600
DB 548 AAGAGGGGTCTCTACACTGTGCGGCGCTGATCCCTACCAAGGCTGCGCGCTGCTG 607
QY 601 TCAATGCTGCGCGCTGCTGCTTCTTCCATTCAGAGCTTCTTACTGATGCTGAGCT 660
DB 608 TCAATGCTGCGCGCTGCTGCTTCTTCCATTCAGAGCTTCTTACTGATGCTGAGCT 667
QY 661 ACTTCTCTGACACATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
DB 668 ACTTCTCTGACACATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 727
QY 721 CTGCTGCTCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
DB 728 CTGCTGCTCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 787
QY 781 ATGGGAAGCCGGAATACAGAACCGGCTGAGCGTGTCTTCAAGTTGTCGCTACGAG 840
DB 788 ATGGGAAGCCGGAATACAGAACCGGCTGAGCGTGTCTTCAAGTTGTCGCTACGAG 847
QY 841 GCTTCTTCAAGCCGCTGAGAGGCTTCAAGCGCTGCTGCTGCTGCTGCTGCTGCTG 900
DB 848 GCTTCTTCAAGCCGCTGAGAGGCTTCAAGCGCTGCTGCTGCTGCTGCTGCTGCTG 907
QY 901 TCTTCACTTCACTTCTTGAAGAGATGAAACAGGCTTCAAGGCTTCTTCTGATG 960
DB 908 TCTTCACTTCACTTCTTGAAGAGATGAAACAGGCTTCAAGGCTTCTTCTGATG 967
QY 961 GCTGAAGCGTTTCAGGCGACACA 983
DB 968 GCTGAAGCGCGCGGCGCTCCCA 990

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RESULT 2
CR606322 1386 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CS0DL003YL12 of B cells (Ramos cell line)
DEFINITION

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ACCESSION Cot 25-normalized of Homo sapiens (human) .
VERSION CR606322
KEYWORDS HTC; CDS; cDNA;
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Molecular Data: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1 (bases 1 to 1386)
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
TITLES Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue
2 (bases 1 to 1386)
REFERENCE Genoscope.
AUTHORS Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
source Location/Qualifiers
1..1386
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DL003YL12"
/issue_type="B cells (Ramos cell line) Cot 25-normalized"
/plasmid="pCMVSPORT_6"
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Query Match 86.3%; Score 968.6; DB 4; Length 1386;
Best Local Similarity 99.1%; Pred. No. 1e-240; 9; Indels 0; Gaps 0;
Matches 974; Conservative 0; Mismatches 9;
QY 1 CCGAGGGCCATTGATGCGATGCGGCGACGCGGATGCGCGGCGGCGGATGAGCG 60
DB 35 CCGAGGGCCATTGATGCGATGCGGCGACGCGGATGCGCGGCGGCGGATGAGCG 94
QY 61 GGAAGCCCGGATCTCCCTTAAGTCCGTCAAGTTCTGTTGGGGGCTGCGCGGATG 120
DB 95 GGAAGCCCGGATCTCCCTTAAGTCCGTCAAGTTCTGTTGGGGGCTGCGCGGATG 154
QY 121 GAGCTACAGTTTGTTCAGCCCGCTGAGCCTGCTGAGAAACCGGATGAGCGGG 180
DB 155 GAGCTACAGTTTGTTCAGCCCGCTGAGCCTGCTGAGAAACCGGATGAGCGGG 214
QY 181 AAGGGCCAAAGACTCGAAGTACAAAACAGCTTCCATGCGCTCACCAGTATCTGAAG 240
DB 215 AAGGGCCAAAGACTCGAAGTACAAAACAGCTTCCATGCGCTCACCAGTATCTGAAG 274
QY 241 CAGAAAGCCCTGAGAGGCGATTATACATGAGCTGCTGCTGCTGCTGCTGCTGCTG 300
DB 275 CAGAAAGCCCTGAGAGGCGATTATACATGAGCTGCTGCTGCTGCTGCTGCTGCTG 334
QY 301 ACACCACTACCCGCTTGGCATCTATACCGTGTGCTTTGAGGCGCTGAGCTGGGCGT 360
DB 335 ACACCACTACCCGCTTGGCATCTATACCGTGTGCTTTGAGGCGCTGAGCTGGGCGT 394
QY 361 GTAATCCCTGCTTCTGCTGAGGCTGCTGATGAGGATGAGCGAGTGCACCTGATG 420
DB 395 GTAATCCCTGCTTCTGCTGAGGCTGCTGATGAGGATGAGCGAGTGCACCTGATG 454
QY 421 CTTTGTGGGAACACACCGGAAAGTGCTTTATCCGATGACTGCCGATGCGCGCTTC 480
DB 455 CTTTGTGGGAACACACCGGAAAGTGCTTTATCCGATGACTGCCGATGCGCGCTTC 514

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 2, 2006, 04:06:54 ; Search time 293.617 Seconds
(without alignments)
9099.175 Million cell updates/sec

Title: US-09-888-264-2

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Sequence: 1 cctcgtgccagcgctgcgcg.....ccaaaaaaaaaaaaaaaa 1503

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	600.4	39.9	11073	3	US-09-949-016-15809 Sequence 15809, A
C 2	497	33.1	2449	3	US-09-949-016-4067 Sequence 4067, Ap
C 3	130.2	8.7	2003	3	US-09-620-312D-874 Sequence 874, App
4	118	7.9	1398	3	US-09-463-229-6 Sequence 6, Appli
5	105.4	7.0	550	3	US-09-669-751-190 Sequence 190, App
6	100.6	6.7	930	3	US-10-001-051B-1 Sequence 1, Appli
7	100.6	6.7	1185	3	US-09-949-016-3539 Sequence 3539, Ap
8	100.6	6.7	1255	2	US-08-518-878B-38 Sequence 38, Appl
9	100.6	6.7	1255	2	US-08-294-522B-38 Sequence 38, Appl
10	100.6	6.7	1255	2	US-08-470-868A-38 Sequence 38, Appl
11	100.6	6.7	1596	2	US-08-807-861A-38 Sequence 38, Appl
12	100.6	6.7	1596	3	US-09-210-681-38 Sequence 38, Appl
13	100.6	6.7	1596	3	US-08-946-719A-38 Sequence 38, Appl
14	100.6	6.7	1596	3	US-09-547-983-38 Sequence 38, Appl
15	100.6	6.7	1949	2	US-08-937-466-3 Sequence 3, Appli
16	100.6	6.7	1949	2	US-09-172-528-3 Sequence 3, Appli
17	100.6	6.7	1949	3	US-09-318-199-3 Sequence 3, Appli
18	100.6	6.7	1949	3	US-09-503-579-3 Sequence 3, Appli
19	99	6.6	2782	2	US-08-937-466-1 Sequence 1, Appli
20	99	6.6	2782	2	US-09-172-528-1 Sequence 1, Appli
21	99	6.6	2782	3	US-09-318-199-1 Sequence 1, Appli
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23	96.8	6.4	1777	2	US-08-937-466-5 Sequence 5, Appli
24	96.8	6.4	1777	2	US-09-172-528-5 Sequence 5, Appli

25	96.8	6.4	1777	3	US-09-318-199-5 Sequence 5, Appli
26	96.8	6.4	1777	3	US-09-503-579-5 Sequence 5, Appli
27	96	6.4	1231	3	US-09-808-457-1 Sequence 1, Appli
28	96	6.4	1231	3	US-09-423-410-3 Sequence 3, Appli
29	96	6.4	2705	3	US-09-949-016-2947 Sequence 2947, Ap
30	95.8	6.4	1351	3	US-09-463-239-27 Sequence 27, Appl
31	94.4	6.3	1192	3	US-09-142-565-1 Sequence 1, Appli
32	91	6.1	924	3	US-09-023-655-890 Sequence 890, App
33	91	6.1	1154	3	US-09-949-016-4550 Sequence 4550, Ap
34	83.8	5.6	1132	3	US-09-808-457-3 Sequence 3, Appli
35	83.8	5.6	1132	3	US-09-423-410-5 Sequence 5, Appli
36	83.6	5.6	512	3	US-09-702-705-1014 Sequence 1014, Ap
37	83.6	5.6	512	3	US-09-736-457-1014 Sequence 1014, Ap
38	83.6	5.6	512	3	US-09-614-124B-1014 Sequence 1014, Ap
39	83.6	5.6	512	3	US-09-671-325-1014 Sequence 1014, Ap
40	83.6	5.6	512	3	US-09-658-824-1014 Sequence 1014, Ap
41	83.6	5.6	512	3	US-10-017-754-1014 Sequence 1014, Ap
42	83.6	5.6	512	3	US-09-651-563-1014 Sequence 1014, Ap
43	80	5.3	1883	3	US-09-774-528-412 Sequence 412, App
44	80	5.3	1883	3	US-10-120-988-412 Sequence 412, App
45	66.8	4.4	816	3	US-10-037-417-25 Sequence 25, Appl

ALIGNMENTS

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RESULT 1
US-09-949-016-15809/c
; Sequence 15809, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 15809
; LENGTH: 11073
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15809
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Best Local Similarity 67.2%; Pred. No. 1.4e-142;
Matches 1286; Conservative 0; Mismatches 6; Indels 622; Gaps 6;
QY      203 CCGGATGGGAGCTACAGTTTGTCCAGCCCTCGACCTGCTGTGAAGAACCGGATGCAGT 262
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DB      3062 CAGGATGGGAGCTACAGTTTGTCCAGCCCTCGACCTGCTGTGAAGAACCGGATGCAGT 3003
      |||
QY      263 TGAGCGGGGAAAGGGCCCAAGACTCGAGATGACAAACAGCTTCATGCCCTGCACAGTA 322
      |||
DB      3002 TGAGCGGGGAAAGGGCCCAAGACTCGAGATGACAAACAGCTTCATGCCCTGCACAGTA 2943
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QY      323 TCCTGAAGGAGAGGCTGAGGGGCAATTACACTG----- 358
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DB      2942 TCCTGAAGGAGAGGCTGAGGGGCAATTACACTGCGGTATTTGGGGCTCAGATGAGAG 2883
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QY      359 ----- 358
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DB      2882 GTAGACTGTGGGTTGGAGCTTACAGCTTGGCTGTATGCTGACCCCTGTCTCTCA 2823
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QY      359 GGCCTGTGGGCTGGCTGTGGCTGTGAGGCACTTACACCACTTGGCTGTCTCTCA 418
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Db      2822 GGCTGTGGGCTGCTGCGCTCAGGCCACCTACCACTACCCGCTTGGACTATATA 2763
QY      419  CCGTGTGTTTGAAGCCCTGACTGAGGGGCTGATGTTACTCCCGCTTGTCTGTAAG 478
Db      2762 CCGTGTGTTTGAAGCCCTGACTGAGGGGCTGATGTTACTCCCGCTTGTCTGTAAG 2703
QY      479  CTGTGATTTGGCATGACCGGAGGTGCCACTGTGTGCTTTGTGGGAAACGACGCGAAGTGG 538
Db      2702 CTGTGATTTGGCATGACCGGAGGTGCCACTGTGTGCTTTGTGGGAAACGACGCGAAGTGG 2643
QY      539  CTCTTATCCGCGATGACTGCGGATGGCC----- 565
Db      2642 CTCTTATCCGCGATGACTGCGGATGGCCGAGTTCGAAGTCTGAACCCCAAGCCC 2583
QY      566  ----- 565
Db      2582 CATTCCTCGAATCTAGAATGAAGAACAGTTTATATCCGGAATCTGGAGCAGAGTGT 2523
QY      566  ----- 565
Db      2522 TTACCTGTTCGACCTTCTTCTTGTGACCTGTGGGCAATCTGTATCTTGACCTCTTTC 2463
QY      566  -----GGCTTCAAGCTGACCAAGCCGCTGTGCTACAAATAATGTTTAACGCC 612
Db      2462 TGCTTCCCAACAGGCTTCCAGCTGACCAAGCCGCTGTGCTACAAATAATGTTTAACGCC 2403
QY      613  CTGATTCGATATCAGCGGGAAGAGGGTGTCTCACACTGTGGCG----- 656
Db      2402 CTGATTCGATATCAGCGGGAAGAGGGTGTCTCACACTGTGGCGGAGTGAAGGAGGCT 2343
QY      657  ----- 656
Db      2342 GGAGACTTGGGGGCTGTAGAGTCTGGTTTTAGGGGTTTTGACTCTTCCCGCTCCCTTC 2283
QY      657  -----GGGCTGATTCCTTACCATGCTGTGGGCGCTGTGTGTAAATGCTGCCAGCTCGC 710
Db      2282 CCTCCAGGCTGTATCCTTACCATGCTGTGGGCGCTGTGTGTAAATGCTGCCAGCTCGC 2223
QY      711  CTCCTACTCCCAATCCAGAGATTCTTACTGACT----- 745
Db      2222 CTCCTACTCCCAATCCAGAGATTCTTACTGACTGACTGAGATCCAGAGCTGGGCGCT 2163
QY      746  ----- 745
Db      2162 TAGTTCCAAGCTGGGCTGAGCCACTGTGAGCTGACTGCCACCCCGCTCACTCCCC 2103
QY      746  CAGGCTACTTCTGTGCAACATCTTGTGCCACTTGTGTGCAGACTGATCAGCGGCTTG 805
Db      2102 CAGGCTACTTCTGTGCAACATCTTGTGTGCCACTTGTGTGCAGACTGATCAGCGGCTTG 2043
QY      806  TCACCACTGTGCTGCATGCTGTGTGGAATTTGCCAAGACCC----- 847
Db      2042 TCACCACTGTGCTGCATGCTGTGTGGAATTTGCCAAGACCCGAGTGTGCAAGCTTG 1983
QY      848  ----- 847
Db      1982 GCCTGAGGTGGGTGGAGGGGTGCCTTTCGATCTCTCATGCCCCGTGCGTCTCTGCG 1923
QY      848  -GAATCAGAAACATGCGGATGATTTATGGGAAGCCGAATACAAAGACGGGCT----- 899
Db      1922 AGAATTCAGAAACATGCGGATGATTTATGGGAAGCCGAATACAAAGACGGGCTGTGAGG 1863
QY      900  ----- 899
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QY      901  GACGTGTCTTTCAAAAGTTGTCCGCTACGAGAGGCTTCTTACGCTGTGTGAAGAGGCTTACAG 960
Db      1742 GACGTGTCTTTCAAAAGTTGTCCGCTACGAGAGGCTTCTTACGCTGTGTGAAGAGGCTTACAG 1683

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QY      1021  AACAAAGCCTTACAAAGGCTCTTCTCTCACTGTGCTGAAGGAGCCGAGGAGCTCCACTGCGC 1080
Db      1622 AACAAAGCCTTACAAAGGCTCTTCTCTCACTGTGCTGAAGGAGCCGAGGAGCTCCACTGCGC 1563
QY      1081  TGCTGGCTTATAGCACACTGGCCCTTGGGGGCTGGGGCTGTGCTGTGCTGGACCCCTTA 1140
Db      1562 TGCTGGCTTATAGCACACTGGCCCTTGGGGGCTGGGGCTGTGCTGTGCTGGACCCCTTA 1503
QY      1141  TTTATTTCCCTTCCACAGTGTGGTTTCTTCTCTGCGGTAAAGAACTTGGTCTGTCTAC 1200
Db      1502 TTTATTTCCCTTCCACAGTGTGGTTTCTTCTCTGCGGTAAAGAACTTGGTCTGTCTAC 1443
QY      1201  CCCCTGTCCAGCTTGGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1260
Db      1442 CCCCTGTCCAGCTTGGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1383
QY      1261  TTGCAAGGAGCTGAAATCTTCTGAGATTTCTGSCCTCCCTGGGTTTATGTTTCA 1320
Db      1382 TTGCAAGGAGCTGAAATCTTCTGAGATTTCTGSCCTCCCTGGGTTTATGTTTCA 1323
QY      1321  GGCAACAGAGCAGAGAAAGATCCCTTGTGCTAGTGGGAAACCAAGAGCAGAGCTGAGGG 1380
Db      1322 GGCAACAGAGCAGAGAAAGATCCCTTGTGCTAGTGGGAAACCAAGAGCAGAGCTGAGGG 1263
QY      1381  GACAGGAGAGCAGAGAACCATCAAGATGTGCAAAAGGCTTGCAGAGGAGATGTGGCC 1440
Db      1262 GACAGGAGAGCAGAGAACCATCAAGATGTGCAAAAGGCTTGCAGAGGAGATGTGGCC 1203
QY      1441  TTCCTCCCTCTGATGAGACTTAATAATTGATTTGATGACCAAAAAAAAA 1494
Db      1202 TTCCTCCCTCTGATGAGACTTAATAATTGATTTGATGACCAAAAAAAAA 1149

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RESULT 2
US-09-949-016-4067/c
; Sequence 4067, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 60/237,768
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4067
; LENGTH: 2449
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4067

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Query Match      33.1%; Score 497; DB 3; Length 2449;
Best Local Similarity 81.3%; Pred. No. 1.7e-116;
Matches 682; Conservative 0; Mismatches 5; Indels 152; Gaps 3;

QY      11  GGGGTGGCGGCGCCCTGCTGTGTGGCGGCGGAGTGTACCTTGGGCGCGAGCGGGGCG 70
Db      689  GGGGTGGCGGCGCCCTGCTGTGTGGCGGCGGAGTGTACCTTGGGCGCGAGCGGGGCG 630
QY      71  GTGCGGCAAGGAGCCCGAGCCGAGGCGCAATTGATGTGCGATGTGCGGCGAGCGAGTG 130

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RESULT 2
US-10-750-623-57090/c
; Sequence 57090, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: PANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57090
; LENGTH: 587
; TYPE: DNA
; ORGANISM: Bovine 1986680933603
US-10-750-623-57090

Query Match 11.0%; Score 165.8; DB 7; Length 987;
Best Local Similarity 93.4%; Pred. No. 1.5e-32;
Matches 184; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

QY 12 GCGTGGCGCGCCCTCG-CTCTGTTCGCGCGCGGTGTCACTTGGGCGGAGCGGCGCC 70
DB 964 GTGCGGCGCGCCCTCGCCCTTGTTCGCGCGGTGTCACTTGGGCGGAGCGGCGCC 905
QY 71 GTGCGGCGAGCGGAGCCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 130
DB 904 GCGCGGCGAGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 845
QY 131 CCGGCGCGCGGCGGAGTGAACCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 190
DB 844 CCGGCGCGCTTCTGGAGTGAACCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 785
QY 191 TTGGGGGCGCTGGCGGCGG 207
DB 784 TTGGGGGCGCTGGCGGCGG 768

RESULT 3
US-11-136-527-3307
; Sequence 3307, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3307
; LENGTH: 1339
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-3307

Query Match 7.9%; Score 118.4; DB 8; Length 1339;
Best Local Similarity 48.0%; Pred. No. 2e-20;
Matches 415; Conservative 0; Mismatches 431; Indels 18; Gaps 2;

QY 178 GTCAAGTTCCTGTGTGGGGGCGCTGGCGCGGATGGAGCTACAGTTTGTGTCCAGCCCTG 237
DB 178 GTAAAGTTCCTGGGGGCGCGGCACTGCAGCTCTTTTGTGTGATCTCTCACTTCCCGCTG 237
QY 238 GACTGTGTGAAGACCGGATGTGAGTGGCGGGA-----AGGGCGAAGCTGTGAAG 291
DB 238 GACACCGGCAAGTCCGCTGTGAGATCCAAAGGGGAAACCCAGAGTGTGACGCTGCAG 297
QY 292 TCAAAAACAGCTTCATGACCTCAACAGTATCTGAAAGGAGGAGGCTGAGGGGCAAT 351
DB 298 TACCGGGGCTGTGTGTGATCACTTGAATGTGTGCGCAGAGAGGTCCCGCAGCCCC 357
QY 352 TACAGGAGCTGTCCGCTGTGCGCTGTGCTGAGGCGACCTACACCACTACCCGCTTGGC 411
DB 358 TACAGGAGCTGTGTGTGCTGTGCGCTGTGCTGATGCGAGATGAGTTTGTCTCCATTTGGAATGGC 417
QY 412 ATCTATACCGTGTCTTTTGAAGCGCTGACTGGGGCTGATGTACTTCCCTGTGCTTTGTG 471
DB 418 CTCTACGACTGTGTCAAGCAGTTCTACACCCCAAGGAACGAGACCACTCCAGCGTCCG 477
QY 472 CTGAAGGCTGTGATTTGGATGACCGAGGTGCGACTGTGTGCTTTGTGTGGAACACAGGC 531
DB 478 ATCAGGATTTGTGCAAGCTGCACCAAGGAGGCGGAGGAGTGAAGCTGTGTCAACCCAGC 537
QY 532 GAAGTGTCTTATCCGATGACTGCGATGCGCGGCTTCCAGCTGACCAAGCGCGGTGGC 591
DB 538 GATGTGTGAAGTGTGATTCGATTTCAAGCATGATACCCCTGTGGAACTGTGAGCGAGGAAA 597
QY 592 TACAAAATGTGTTTAAGCGCTGTGATTTGATATCCCGGAAAGAGGTGTCTCAACTGT 651
DB 598 TACAGAGGAGTATGATGCTTACAGAAACATGCGCAGGAGGAAAGAGTCAAGGAGACTGTG 657
QY 652 TGGCGGGGCTGTGATCCCTACCAAGCTGTGGGCGGTGTGTGTAATGTGCGGCGGCGCC 711
DB 658 TGGAAAGGACTTGGCCCAACATCAAGAAAGCGCATTTGTAATGTGTGTGAGATGTGTG 717
QY 712 TCTTACTCCCATCCAGCAGTTCTTACTGACTGAGCTGACTTCTGTGCAACAATCTTGT 771
DB 718 ACTTATGACATCATGAAGAGAGAGTGTGCTGACTTCACTGTCTCACTGTGCAACTTCCCG 777
QY 772 TGCACCTTCTGTGCAAGATGATCAGCGTCTTGTGCACCACTGTGCTCTCATGCTGTGTG 831
DB 778 TGTCACTTGTCTGTGCTTGTGAGCTGTGTGTGTGTGCAAGTGTGTGTGCTTCCCGAGTG 837
QY 832 GACATTTGCCAAGACCGGAATCCAGAAATGCGGATGTGATGGGAAGCCGGAATAACAAG 891
DB 838 GATGTGTGAAGACCCGATAC-----ATGAACGCTCTCCCGCAGGAGTACCGA 885
QY 892 AACGGGCTGACGCTGTCTTCAAGTTGTCCGCTACGAGGCGTTCTTCAAGCTGTGAAG 951
DB 886 AGCCCCCTTACACTGTATGTGTGAGATGTGTGCGCCAGAGAGGCCCCACAGCTTCTACAAA 945
QY 952 GCGTTTCAAGCGCTTATGTCCGCGCTGTGGCGCCCGCACACGCTCTCACTTCACTTCTTGT 1011
DB 946 GGATTCATGCGCTCTTCTGTGTGTGTGGGATCTGGAACGTATATGTGTGTATTAACCTTAC 1005
QY 1012 GAGCAGATGAACAAGGCTTACAAAG 1035
DB 1006 GAGCAGCTGAACGGGCTTGTATG 1029

RESULT 4
US-11-010-239-108
; Sequence 108, Application US/11010239
; Publication No. US20060015970A1
; GENERAL INFORMATION:
; APPLICANT: Roger PENNELL
; APPLICANT: Jack OKAMURO
; APPLICANT: Richard SCHNEBERGER
; APPLICANT: Yiwen FANG
; APPLICANT: Shing KWOK
; APPLICANT: Diane JOFUKU

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OM nucleic - protein search, ~~us09-888-264-2~~ model

Run on: February 1, 2006, 13:19:02 ; Search time 47.9632 Seconds
(without alignments)
2753.720 Million cell updates/sec

Title: US-09-888-264-2

Sequence: 1 cctcgtgccagcgtgcgcg.....ccaaaaaiaaaaaaaaaa 1503

Scoring table:

BLSUM62	
Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 4886326

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=A/abes/AASSWB_epool/US09888264/unat_01022006_11837_14767/app_query.fasta_1
-UNITS=bits -START=1 -END=1 -MATRIX=blsum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pic -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs802p
-USER=US09888264@CGN 1 1 476 @unat 01022006 11837 14767 -NCPU=6 -ICPU=3
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-WARN TIMEOUT=30 -THRAUS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A/Genesep21:*

1: genesep21980s:*
2: genesep21980s:*
3: genesep22000s:*
4: genesep22001s:*
5: genesep22002s:*
6: genesep22003as:*
7: genesep22003bs:*
8: genesep22004s:*
9: genesep22005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1603	56.3	314	7	ABG75060 Human sol
2	1603	56.3	314	7	AD163106 Human apo
3	1603	56.3	314	7	ADJ71209 Human hea
4	1603	56.3	314	7	ADJ70398 Human hea
5	1603	56.3	314	8	ADQ89940 Antagonis
6	1600	56.2	314	7	ADJ68692 Human hea
7	1579	55.5	342	7	ADG31772 Human nov
8	1579	55.5	342	8	ADJ27213 Human TRI
9	1311.5	46.1	263	8	ADJ27204 Human TRI

10	1060	37.2	312	8	ADX97090	Adx97090 plant ful
11	1058.5	37.2	323	8	ADN22668	Adn22668 Bacterial
12	946	33.2	314	9	ADY64720	Ady64720 S. manson
13	919.5	32.3	317	4	ABBS8008	Abbs8008 Drosophila
14	840.5	29.5	311	4	ABBS6966	Abbs6966 Drosophila
15	781	27.4	301	4	ABBS7921	Abbs7921 Drosophila
16	781	27.4	301	8	ADQ89738	Adq89738 Antagonis
17	776.5	27.3	178	8	ADN33130	Adn33130 Human tra
18	606	21.3	306	7	ABW73602	Abw73602 DNA clone
19	603.5	21.2	344	8	ADX78358	Adx78358 plant ful
20	602.5	21.2	349	8	ADX78463	Adx78463 plant ful
21	592.5	20.8	305	8	ADY07225	Ady07225 plant ful
22	591	20.8	298	8	AAQ09948	Aaq09948 Arabidops
23	589	20.7	341	8	ADX89570	Adx89570 plant ful
24	585.5	20.6	285	8	ADX72228	Adx72228 plant ful
25	583	20.6	313	3	AAQ50517	Aaq50517 Arabidops
26	579	20.3	313	3	AAQ19643	Aaq19643 Arabidops
27	568.5	20.0	273	3	AAQ09949	Aaq09949 Arabidops
28	554	19.5	313	3	AAQ49736	Aaq49736 Arabidops
29	554	19.5	313	3	AAQ29874	Aaq29874 Arabidops
30	554	19.5	341	3	AAQ49735	Aaq49735 Arabidops
31	554	19.5	342	3	AAQ29873	Aaq29873 Arabidops
32	537.5	18.9	262	3	AAQ09950	Aaq09950 Arabidops
33	535	18.8	284	3	AAQ50518	Aaq50518 Arabidops
34	531	18.7	284	3	AAQ19644	Aaq19644 Arabidops
35	525	18.4	276	8	ADS23506	Ads23506 Bacterial
36	516.5	18.1	272	8	ADN20798	Adn20798 Bacterial
37	513.5	18.0	237	3	AAQ50519	Aaq50519 Arabidops
38	510	17.9	230	8	ADN24153	Adn24153 Bacterial
39	509.5	17.9	237	3	AAQ19645	Aaq19645 Arabidops
40	507.5	17.8	302	4	AAQ41612	Aaq41612 Human pol
41	506	17.8	325	3	AAQ44669	Aaq44669 Murine un
42	505	17.7	322	3	AAQ44668	Aaq44668 Murine un
43	504.5	17.7	280	4	ABBS5868	Abbs5868 Drosophila
44	504.5	17.7	280	4	ABBS71693	Abbs71693 Drosophila
45	503.5	17.7	287	4	AAQ36444	Aam36444 Human pol

ALIGNMENTS

RESULT 1

ID ABG75060 standard; protein; 314 AA.

XX AC ABG75060;

DT 12-FEB-2004 (first entry)

DE Human solute carrier family 25 member 11 protein.

XX KW Energy homeostasis; mouse; metabolism; triglyceride; metabolic disease;
gene therapy; anorectic; immunomodulator; antidiabetic; hypotensive;
cardiac; osteopathic; antilipemic.

OS Homo sapiens.

PN W02003075945-A2.

PD 18-SEP-2003.

PF 14-MAR-2003; 2003WO-EP002714.

PR 14-MAR-2002; 2002EP-00005882.

PR 15-MAR-2002; 2002EP-00006012.

PR 20-MAR-2002; 2002EP-00006271.

PR 25-MAR-2002; 2002EP-00006810.

PA (DEVE) DEVELOPMENTAL BIOLOGISCHE FORSCH.

PI Eulenberg K, Steuernagel A, Haeder T, Broenner G;
WPI; 2003-748334/70.

DR N-PSDB; ACH00820.

XX New pharmaceutical composition comprising a nucleic acid molecule
 PT encoding proteins regulating the energy homeostasis and metabolism of
 PT triglycerides useful for detecting or preventing metabolic diseases, e.g.
 PT obesity.

XX Claim 3; Fig 11C; 140pp; English.

XX The present invention relates to pharmaceutical compositions comprising
 CC the coding sequences shown in ACH00815-ACH00827, or their encoded
 CC proteins (known in ABG75054, ABG75056-ABG75067). These are proteins
 CC involved in the metabolism of triglycerides and in energy homeostasis,
 CC and their coding sequences. The composition is useful for the manufacture
 CC of an agent for detecting, verifying, treating, alleviating or preventing
 CC disorders, including metabolic diseases such as obesity and other body-
 CC weight regulation disorders as well as related disorders such as
 CC metabolic syndrome, eating disorder, cachexia, diabetes mellitus,
 CC hypertension, coronary heart disease, hypercholesterolemia,
 CC dyslipidaemia, osteoarthritis or gallstones, in cells, cell masses,
 CC organs or subjects. The coding sequences can be used in the production of
 CC transgenic animals which under- or over-produce the gene of interest. The
 CC present sequence is a protein of the invention

XX Sequence 314 AA:

SQ

Alignment Scores:
 Pred. No.: 3,97e-128 Length: 314
 Score: 1603.00 Matches: 314
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 56.3% Indels: 0
 DB: 7 Gaps: 0

US-09-888-264-2 (1-1503) x ABG75060 (1-314)

QY 112 ATGGCGGCGAGCGGAGTCCGGGCGCGGAGTACGCGGAAGCCCGTACCTCCCT 171
 DB 1 MetAlAlaThrAlaSerAlaGlyAlaGlyAlaAspIlySerProArgThrSerPro 20
 QY 172 AACTCGGTCAAGTCCGTTGGGGGCGTGGCGGAGTGGAGCTACAGTTTGGCGAG 231
 DB 21 LysSerValLysPheLeuPheGlyGlyLeuAlaGlyMetCylValThrValPheValGln 40
 QY 232 CCCCTGACCTGGTGAAGAACCGGATGCAAGTTGAGCGGAGGCGCAAGACTCGAGAG 291
 DB 41 ProLeuAspLeuValLysAsnArgMetGlnLeuSerCylGlnIlyAlaIyThrArgGln 60
 QY 292 TACAAACCAAGCTTCCATGCGCTCCACCAAGTATCTTGAAGGAGAGGCTGAGGGGCAAT 351
 DB 61 TyrLysThrSerPheHisAlaLeuThrSerIleLeuLysAlaGlnIlyLeuArgGlyIle 80
 QY 352 TACACTGGGCGTGGCGTGGCGTGGCGTGGCGGACCACTCCACCACTCCGCGCTGGC 411
 DB 81 TyrThrGlyLeuSerAlaGlyLeuLeuArgGlnAlaThrThrThrThrArgLeuGly 100
 QY 412 ATCTATACCGTGTGTTTGAAGCGCTGACTGAGGGCTGATGATGATCCCTCGGCTTCTG 471
 DB 101 IleTyrThrValLeuPheGlnArgLeuThrCylAlaAspIlyThrProProGlyPheLeu 120
 QY 472 CTGAAGGCTGTGATTGGCATGACCGGAGTGCACCTGTGCTTTGTGGAAACACAGCC 531
 DB 121 LeuLysAlaValIleGlyMetThrAlaGlyAlaThrCylAlaPheValGlyThrProAla 140
 QY 532 GAAGTGGCTTTATCCGATGACTGCGGATGGCGGCTTCCAGCTGACCGCGCGCTGGC 591
 DB 141 GluValAlaLeuIleArgMetThrAlaAspGlyArgLeuProAlaAspGlnArgArgGly 160
 QY 592 TACAAATATGTGTTTAAAGCGCTGATTGCAATCACCGGGAAGAGGCTGCTCACAGC 651
 DB 161 TyrLysAsnValPheAsnAlaLeuIleArgIleThrArgIlyGlnIlyValLeuThrLeu 180
 QY 652 TGGCGGGCTGATCCCTACCATGAGCTGGGGCGTCTCTGTCATAGTGTGCCAGCTGACC 711

DB 181 TrpArgGlyCysIleProThrMetAlaArgAlaValAlaAsnAlaAlaGlnLeuAla 200
 QY 712 TCTACTCCCAATCCAGAGATTCTTACTGACTGAGCTACTTCTTGACAACATCTTG 771
 DB 201 SerTyrSerGlnSerIlySerGlnPheLeuLeuAspSerGlyTyrPheSerPheIleLeu 220
 QY 772 TSCCACTTGTGCGAGCATGATCAGCGGCTTTGTCCACCACTGCTCCATGCTGTG 831
 DB 221 CysHisPheCysAlaSerMetIleSerGlyLeuValThrThrAlaIleSerMetProVal 240
 QY 832 GACATTGCCAAGAACCCGGAATCCAGAACATGCGGATGATGAGGAGCGGAATPACAAG 891
 DB 241 AspIleAlaLysThrArgIleGlnIleAsnMetArgMetIleAspGlyLysProGlyLys 260
 QY 892 AACGGGCTGAGGTGCTGTTCAAGATTGTCGCGCTACGAGGGCTTCTTCAGCTGTGGAAG 951
 DB 261 AsnGlyLeuAspValLeuPheLysValAlaArgTyrGlnIlyPhePheSerLeuTrpLys 280
 QY 952 GCGTTACGCGGCTACTGAGCCGCGCTGGGCGCCACACCGTCTCATCTTATCTTGG 1011
 DB 281 GlyPheThrProTyrTyrAlaArgLeuGlyProHisThrValLeuThrPheIlePheLeu 300
 QY 1012 GAGCAGATGACAGAGCCCTACAGAGCTCTTCTTCCAGTGGC 1053
 DB 301 GluGlnMetCAsnLysAlaTyrLysArgLeuPheLeuSerGly 314

RESULT 2
 ADI63106
 ID ADI63106 standard; protein; 314 AA.
 XX ADI63106;
 AC
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Human apoptosis-associated protein SEQ ID 549.
 XX
 KW apoptosis; cell death; cytoskeletal; neuroprotective; immunosuppressive;
 KW antithrombotic; antiarthritic; dermatological; antiinflammatory;
 KW hepatotropic; virucide; nootropic; anticonvulsant; antiparkinsonian;
 KW vasotropic; cerebroprotective; antialcoholic; gene therapy; tumour;
 KW autoimmune diseases; degenerative disease; viral infection; leukaemia;
 KW lupus; hepatitis; influenza viruses; rheumatoid arthritis; diabetes;
 KW Huntington's disease; Parkinson's diseases; reperfusion injury; stroke;
 KW alcoholic liver disease; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2003058021-A2.
 XX
 PD 17-JUL-2003.
 XX
 PF 13-JAN-2003; 2003WO-BP000270.
 XX
 PR 11-JAN-2002; 2002DE-01000856.
 XX
 PA (XANT-) XANTOS BIOMEDICINE AG.
 XX
 PI Koenig-Hoffman K, Kazinski M, Schaefer R, Kasper B;
 XX
 DR WPI; 2003-542334/51.
 XX
 PT New nucleic acids involved in apoptosis, useful for diagnosis and
 PT treatment of e.g. tumors and degenerative disease, also related proteins,
 PT antibodies and modulators.
 XX
 PS Claim 1b; SEQ ID NO 549; 517bp; German.
 XX
 CC This invention describes novel nucleic acid molecules that are associated
 CC with apoptosis and encode a polypeptide and are derived from a normalised
 CC gene library (embryonic or liver) or clone collections, and the extent of
 CC apoptosis measured by cell death detection assay or the CERG assay
 CC (measuring loss of membrane integrity). The products of the invention

GenCore version 5.1.7
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OM nucleic - protein search, using frame_plus_n2p model

Run on: February 1, 2006, 13:33:41 ; Search time 11.0464 Seconds
(without alignments)
2618.292 Million cell updates/sec

Title: US-09-888-264-2

Sequence: 1 cctcgtccagcgtcgcgcg.....ccaaaaaaaaaaaaaaaaa 1503

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=PIR -QMT=faetan -SUFFIX=rxpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=Dlosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pic -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs02p
-USER=US09888264 @CCN.1.1.77@runat.01022006.11840.14810 -NCPU=6 -ICPU=3
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-MAIN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

PIR 80:*
1: pirl:*
2: pirl:*
3: pirl:*
4: pirl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1600	56.2	314	2	A56650 2-oxoglutarate car
2	1545	54.3	314	2	A36305 2-oxoglutarate/mal
3	1058.5	37.2	323	2	T25459 hypothetical prote
4	602.5	21.2	302	2	S65040 2-oxoglutarate/mal
5	598	21.0	302	2	S65042 2-oxoglutarate/mal
6	584.5	20.5	297	2	T07405 oxoglutarate/malat
7	583	20.5	313	2	D84613 hypothetical prote
8	554	19.5	313	2	T05577 uncoupling protein
9	527.5	18.5	331	2	T51899 probable 2-oxogluc
10	510	17.9	290	2	S44091 oxoglutarate/malat
11	498	17.5	325	2	JC7553 brain mitochondria
12	468	16.4	305	2	H86274 F7A19.22 protein -
13	459.5	16.1	298	2	S51351 hypothetical prote
14	445.5	15.6	282	2	T49628 probable dicarboxy

15	438.5	15.4	307	2	G01858 uncoupling protein
16	434.5	15.3	306	2	T07793 uncoupling protein
17	426	15.0	312	2	JC5522 uncoupling protein
18	422.5	14.8	307	2	A26294 uncoupling protein
19	415.5	14.6	306	2	A31106 mitochondrial unco
20	415.5	14.6	307	2	S34268 uncoupling protei
21	413	14.5	320	2	T37603 probable oxalacet
22	411.5	14.5	306	2	T47570 uncoupling protein
23	402.5	14.1	306	2	T52024 uncoupling protein
24	400	14.0	306	2	A32446 uncoupling protei
25	365	12.8	288	2	S03603 mitochondrial unco
26	357.5	12.6	324	2	S25357 mitochondrial prote
27	331	11.6	343	2	T15253 probable carrier p
28	302	10.6	322	2	S57116 probable phosphate
29	280.5	9.9	307	2	S60949 hypothetical prote
30	270.5	9.5	309	2	T48156 hypothetical prote
31	264.5	9.3	702	2	T16533 adenylyate transloc
32	257	9.0	392	2	T05350 probable membrane
33	256.5	9.0	310	2	S69050 mitochondrial solu
34	247	8.7	352	2	T01729 Btl protein precur
35	238	8.4	436	2	U01459 probable peroxisom
36	233.5	8.2	331	2	F84823 peroxisomal Ca-dep
37	232	8.1	475	2	T50686 envelope protein l
38	231.5	8.1	358	2	T09109 probable carrier p
39	231.5	8.1	377	2	S36081 citrate transport
40	228	8.0	289	2	S44554 hypothetical prote
41	224.5	7.9	335	2	S50453 hypothetical prote
42	223.5	7.9	415	2	T48171 probable carrier p
43	223	7.8	902	1	S54495 probable tricarbox
44	221	7.8	291	2	T37992 citrate transporte
45	220.5	7.7	311	2	G01789

ALIGNMENTS

RESULT 1

A56650 2-oxoglutarate carrier protein - human
C/Species: Homo sapiens (man)
C/Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C/Accession: A56650; S29598
C/Ricobazzzi, V.; Palmieri, F.; Runswick, M.J.; Walker, J.E.
DNA Seq. 3, 79-88, 1992
A/Title: Sequence of the human and bovine genes for the mitochondrial 2-oxoglutarate ca.
A/Reference number: A56650; M01D:93091249; PMID:1457818
A/Accession: A56650
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-314 <IAC>
A/Cross-references: UNIPROT:Q02978; UNIPARC:UPI000016A206; EMBL:X66114; NID:q23843; PIDN
A/Note: sequence extracted from NCBI backbone (NCBI:P:120085)
C/Genetics:
A/Intons: 32/2; 83/2; 152/2; 182/3; 246/2; 263/3
C/Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C/Keywords: duplication; mitochondrion; transmembrane protein
F/18-109/Domain: ADP,ATP carrier protein repeat homology <ACPI>
F/116-209/Domain: ADP,ATP carrier protein repeat homology <AC2>
F/216-307/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Alignment Scores:

Pred. No.: 4.44e-105 Length: 314
Score: 1600.00 Matches: 313
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 99.7% Mismatches: 0
Query Match: 56.2% Indels: 0
DB: Gaps: 0

US-09-888-264-2 (1-1503) x A56650 (1-314)

OY 112 ATGCGCGGACGCGGAGTGGCGGCGCGGATAGACGGGAAAGCCCGTACCTCCCT 171
DB 1 MetlaiaatrrAlaseeAlaglyAlaglyolylmetAepglyLvsPProAArgThserPro 20

```

QY 172 AAGTCCGTCAGTCTCTGTTGGGGGCTGGCCGGAGTGAGGACCTACAGTTTGTGCCAG 231
DB 21 LysSerValLysPheLeuPheGlyGlyLeuAlaGlyMetCylValLeuThrValPheValGln 40
QY 232 CCCCTGACCTGGTGAAGAAGCCGATGACGTTGAGGGGGGAAGGGGCAAGACTCGAGAG 291
DB 41 ProluaspLeuValLysasnArgMetGlnLeuSerGlyGlnValAlaLysThrArgGlu 60
QY 292 TACAAAACAGAGCTTCATGCCCTCACCAGATCTCTGAAGGACAGAAAGCCCTGAGGGGCAAT 351
DB 61 TyrLysThrSerPheHisAlaLeuThrSerIleLeuLysAlaGluGlyLeuArgGlyIle 80
QY 352 TACACTGGGCTGTGGCTGGCTGGCTGGCTGAGGCCACTACACCACTACCCGCTTGGC 411
DB 81 TyrThrGlyLysSerLysGlyLeuLeuArgGlnAlaThrYrThrThrThrArgLeuGly 100
QY 412 ATCTATACGGTGTGTTTGAAGGCTGAGCTGGGGCTGAGTGTCTCCCTGGCTTTCG 471
DB 101 LLeYrThrValLeuPheGlnArgLeuThrGlyAlaAspGlyThrProGlyPheLeu 120
QY 472 CTGAAGGCTGTGATGGCATGACCGAGGCTGCTGAGCTGTGCTTGTGGGAACACGAGCC 531
DB 121 LeuLysAlaValIleGlyMetThrAlaGlyAlaThrGlyAlaPheValGlyThrProAla 140
QY 532 GAAAGGCTCTTATTCGCGATGACTGCGCGATGGCGGCTTCAGCTGACCGCGCTGGCC 591
DB 141 GluValAlaLeuLeuLeuArgMetThrAlaAspGlyArgLeuProAlaAspGlnArgArgGly 160
QY 592 TACAAAAGTGTGTTTAAAGCCCTGATTCGAATCAACCGGGGAAGAGGTGTCTTCACACTG 651
DB 161 TyrLysAsnValPheAsnAlaLeuIleArgGlyLeuThrArgGlnGluGlyValLeuThrLeu 180
QY 652 TGGCGGGGCTGATCCCTCATCATGAGCTGGGGCGCTGCTGCTCAATGCTGCCAGCTGGCC 711
DB 181 TrpArgGlyCysIleLeuProThrMetAlaArgAlaValValAlaAsnAlaAlaGlnLeuAla 200
QY 712 TCTACTCCCAATTCAGACAGTCTTACTGAGTCAAGCTACTCTTCTGACCAATCTTG 771
DB 201 SerTyrSerGlnSerIysGlnPheLeuLeuAspSerGlyTyrPheSerAspAsnIleLeu 220
QY 772 TGGCAATTTCTGTGGCCAGCATGATCAGCGGTCTTGTTCACCACTGCTGCTTCATGCTGTG 831
DB 221 CysHisPheCysLysAsnMetIleSerGlyLeuValThrThrAlaAlaSerMetProVal 240
QY 832 GACATTCGCAAGACCCGGAATCCAGAACATGCGGATGATGATGAGGAAGCCGGAATCAAG 891
DB 241 AspIleAlaLysThrArgIleGlnAsnMetArgMetIleAspGlyLysProGlnIlyTrlys 260
QY 892 AACGGGCTGACGCTGTCTTCAAAAGTTGTCCGCTACGAGGGCTTCTTCAAGCTGTGGAAG 951
DB 261 AsnGlyLeuAspValLeuPheLysValValArgTyrGluGlyPhePheSerLeuTrpLys 280
QY 952 GCGTTTACGCGCGTACTATGCGCGCTGGGGCCCCCAACAGCTCTCATCTTCTTGG 1011
DB 281 GlyPheThrProGlyTyrAlaArgLeuGlyProHisThrValLeuThrPheIlePheLeu 300
QY 1012 GAGCAGATGAACAAGGCTACAAAGCGTCTCTTCTTCAAGTGGC 1053
DB 301 GluGlnMetAsnLysAlaTyrLysArgLeuPheLeuSerGly 314

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RESULT 2
A36305
2-oxoglutarate/malate carrier protein, inner mitochondrial membrane - bovine

C:Species: Bos primigenius taurus (cattle)
C:Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #ext change 09-Jul-2004

C:Accession: A36305; B56650; S65731; A54249; S71377; S29597
R:Runswick, M.J.; Walker, J.E.; Bisaccia, F.; Iacobazzi, V.; Palmieri, F.

Biochemistry 29, 11033-11040, 1990
A:Title: Sequence of the bovine 2-oxoglutarate/malate carrier protein: structural relati

A:Reference number: A36305; MUID:91105033; PMID:2271695
A:Accession: A36305
A:Status: preliminary
A:Molecule type: mRNA

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A:Residues: 1-314 <RUN>
A:Cross-references: UNIPROT:P22292; UNIPARC:UPI0000167C3C; GB:M60662; GB:J05296; NID:g16;
R:Iacobazzi, V.; Palmieri, F.; Runswick, M.J.; Walker, J.E.
DNA Seq. 3, 79-88, 1992
A:Title: Sequences of the human and bovine genes for the mitochondrial 2-oxoglutarate car
A:Reference number: A56650; MUID:93091249; PMID:1457818
A:Accession: B56650
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-314 <IA2>
A:Cross-references: UNIPARC:UPI0000167C3C; EMBL:566115; NID:g31; PIDN:CAA46906.1; PID:g3;
R:Iacobazzi, F.; Zera, V.; Capobianco, L.; Iacobazzi, V.; Mazzeo, M.; Palmieri, F.
Biochim. Biophys. Acta 1292, 281-288, 1996
A:Title: The formation of a disulfide cross-link between the two subunits demonstrates t
A:Reference number: S65731; MUID:96176856; PMID:8597574
A:Accession: S65731
A:Status: preliminary
A:Molecule type: protein
A:Residues: 148-160 <B18>
A:Cross-references: UNIPARC:UPI0000177A24
R:Bisaccia, F.; Capobianco, L.; Brandolin, G.; Palmieri, F.
Biochemistry 33, 3705-3713, 1994
A:Title: Transmembrane topography of the mitochondrial oxoglutarate carrier assessed by i
A:Reference number: A54249; MUID:94190892; PMID:8142370
A:Accession: A54249
A:Status: preliminary
A:Molecule type: protein
A:Residues: 6-15;23-32;40-49;62-71;104-113;170-179;183-192 <B12>
A:Cross-references: UNIPARC:UPI000177A25; UNIPARC:UPI0000177A26; UNIPARC:UPI0000177A27;
R:Bisaccia, F.; Capobianco, L.; Mazzeo, M.; Palmieri, F.
FEBS Lett. 392, 54-58, 1996
A:Title: The mitochondrial oxoglutarate carrier protein contains a disulfide bridge betw
A:Reference number: S71377; MUID:96354876; PMID:8769314
A:Accession: S71377
A:Molecule type: protein
A:Residues: 148-160;189-200 <B1W>
A:Cross-references: UNIPARC:UPI0000177A24; UNIPARC:UPI0000177A2C
A:Experimental source: heart
C:Genetics:
A:Intons: 32/2, 83/2, 246/2, 263/3
C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
C:Keywords: duplication; mitochondrion; transmembrane protein
F:18-109/Domain: ADP/ATP carrier protein repeat homology <ACPI>
F:116-209/Domain: ADP/ATP carrier protein repeat homology <ACP2>
F:216-307/Domain: ADP/ATP carrier protein repeat homology <ACP3>
F:221-224/Disulfide bonds: #status experimental

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Alignment Scores:

Pred. No.:	3,38e-101	Length:	314
Score:	1545.00	Matches:	302
Percent Similarity:	97.1%	Conservative:	3
Best Local Similarity:	96.2%	Mismatches:	9
Query Match:	54.3%	Indels:	0
DB:	2	Gaps:	0

US-09-888-264-2 (1-1503) x A36305 (1-314)

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DB 1 MetAlaAlaThrAlaSerProGlyLysArgMetAspGlyLysProArgThrSerPro 20
QY 172 AAGTCCGTCAGTCTCTGTTGGGGGCTGGCCGGAGTGAGGACCTACAGTTTGTGCCAG 231
DB 21 LysSerValLysPheLeuPheGlyGlyLeuAlaGlyMetCylValLeuThrValPheValGln 40
QY 232 CCCCTGACCTGGTGAAGAAGCCGATGACGTTGAGGGGGGAAGGGGCAAGACTCGAGAG 291
DB 41 ProluaspLeuValLysasnArgMetGlnLeuSerGlyGlnValAlaLysThrArgGlu 60
QY 292 TACAAAACAGGTTCCATGCCCTCACCAGATCTCTGAAGGACAGAAAGCCCTGAGGGGCAAT 351
DB 61 TyrLysThrSerPheHisAlaLeuThrSerIleLeuLysAlaGluGlyLeuArgGlyIle 80

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QY 172 AAGTCCGCAAGTCTCTGTTGGGGGCTGGCCGGATGGAGCTACAGTTTGTCCAG 231
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Db 101 TTTTThrValIleuPheGlnArgLeuThrGlyAlaAspGlyThrProGlyPheLeu 120
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Db 121 LeuValaValIleGlyMetThrAlaGlyAlaThrGlyAlaPheValGlyThrProAla 140
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Db 141 GlnValaIaLeuLeuArgMetThrAlaAspGlyArgLeuProAlaAspGlnArgGly 160
QY 592 TACAAATATGTGTTTAAACCGCTGATTCGATTCGACCCGGAGAGGGGTCTCTACACTG 651
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Db 181 TTPATGAGlyCysIleProThrMetAlaArgAlaValaValaValaAsnAlaGlnLeuAla 200
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QY 772 TGGCACTTGTGTGCGACATGATGACGGCTTTGTGACCACTGCTGCTTCATCTGTG 831
Db 221 CysHlaPheCysAlaSerMetIleSerGlyLeuValIleThrAlaAlaSerMetProVal 240
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Db 241 AspIleAlaIysThrArgIleGlnAsnMetArgMetIleAspGlyIysProGlyTyrLys 260
QY 892 AACGGGCTGAGCGTGTGTTCAAGTTGTCCGCTACGAGGGCTTCTTCAAGCTGTGGAAG 951
Db 261 AsnGlyLeuAspValIleuPheIysValIaArgTyrGlyGlyIlePhehSerLeuThrPlys 280
QY 952 GGCCTTACGCGCTACTATGCGCCGCTGGGCGCCACACCGCTCTCACTTCTTCTTG 1011
Db 281 GlyPheThrProTyrTyrAlaArgLeuGlyProhIleThrValLeuThrPheIlePheLeu 300
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Db 301 GlnGlnMetAsnIysAlaTyrLysArgLeuPheLeuSerGly 314

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RESULT 2

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M2OM_HUMAN STANDARD; PRT; 313 AA.
ID M2OM_HUMAN 002378; 075537; 0969P7;
AC 01-JUL-1993 (Rel. 26, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 13-SEP-2005 (Rel. 48, Last annotation update)
DE Mitochondrial 2-oxoglutarate/malate carrier protein (OGCP) (Soluble
DE carrier family 25 member 11).
DE Name=SLC25A11; Synonyms=SLC20A4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Molesteostomi;

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OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93091249; PubMed=1457818;
RA Iacobazzi V., Palmieri F., Runswick M.J., Walker J.E.;
RT "Sequences of the human and bovine genes for the mitochondrial 2-
RT oxoglutarate carrier."
RL DNA Seq. 3:79-88(1992).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC Tissue=Brain;
RL Yu W., Gibbs R.A.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Muscle, and Uterus;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Pangloss S.J.,
RA Roha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Millaby S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunnarone P.H.,
RA Richardson S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP PROTEIN SEQUENCE OF 1-16, CLEAVAGE OF INITIATOR METHIONINE,
RP ACETYLATION SITE ALA-1, AND MASS SPECTROMETRY.
RC TISSUE=B-cell lymphoma;
RA Bienvenu M.V.;
RL Unpublished observations (JUN-2005).
CC -1- FUNCTION: Catalyzes the transport of 2-oxoglutarate across the
CC inner mitochondrial membrane in an electroneutral exchange for
CC malate or other dicarboxylic acids, and plays an important role in
CC several metabolic processes, including the malate-aspartate
CC shuttle, the oxoglutarate/isocitrate shuttle, in gluconeogenesis
CC from lactate, and in nitrogen metabolism.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC -1- SIMILARITY: Contains 3 Solcar repeats.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
DR EMBL; X6114; CAA46905.1; -; Genomic DNA.
DR EMBL; AF070548; AAC28637.1; -; mRNA.
DR EMBL; BC006508; AAH06508.1; -; mRNA.
DR EMBL; BC006519; AAH06519.1; -; mRNA.
DR EMBL; BC016294; AAH16294.1; -; mRNA.
DR EMBL; BC017170; AAH17170.1; -; mRNA.
DR PIR; A56650; A56650.
DR Ensembl; ENSG00000108528; Homo sapiens.
DR HGNC; HGNC:10981; SLC25A11.
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Qy      601 GTGTTTAAGCGCGCTGATTCGATTCACCGGGAAGAGGCTGCTCTCACTGTGGCGGCG 660
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Qy      721 CAATCCAGACGTTCTTACTGAC-----TCAGGCTACTTCTCTGACAAACATCTTG 771
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RESULT 2
US-09-248-796A-17621
; Sequence 17621, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13

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; LENGTH: 313
; TYPE: prt
; ORGANISM: Candida albicans
US-09-248-796A-17621

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US-09-888-264-2 (1-1503) x US-09-248-796A-17621 (1-313)

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Db      70 LeuThrAlaSerLeuLeuArgGlnIleAlaThrIleThrIleArgPheGlyIleIleIleIle 89
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Qy      460 CCTGCGCTTCTGCTGAGGCTGCTGATGGCATGACCGGAGGCTGCTGCTGCTGCTGCTG 519
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GenCore version 5.1.7
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OM nucleic - protein search, using frame_plus_n2p model

Run on: February 1, 2006, 14:41:42 ; Search time 45.3876 Seconds
(without alignments)
2767.263 Million cell updates/sec

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Delop 6.0 , Delext 7.0

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Total number of hits satisfying chosen parameters: 3735138

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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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-LOPCL=0 -LOPEXT=0 -UNITS=bites -START=1 -END=-1 -MATRIX=bl0sum62
-TRANS=numa40.cdi -LIST=45 -DCCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=plo -NORM=ext -HBAFSIZE=500 -MINLEN=0
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-USER=US09888264.@CN 1.1.405 @runat_01022006_11847_14955 -NCPU=6 -ICPU=3
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-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7
-Ygapop=10 -Ygapext=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications_AA.Main:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query length	DB ID	Description
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2	1603	56.3	314	4	US-10-408-765A-3015 Sequence 3015, Ap
3	1603	56.3	314	5	US-10-507-617-13 Sequence 13, Appl
4	1603	56.3	314	5	US-10-745-237-370 Sequence 370, Appl
5	1600	55.2	314	4	US-10-408-765A-498 Sequence 498, Appl
6	1554	54.6	314	5	US-10-507-617-57 Sequence 57, Appl
7	1517	53.3	297	5	US-10-507-617-56 Sequence 56, Appl
8	1060	37.2	310	4	US-10-425-115-211662 Sequence 211662, A
9	1060	37.2	312	4	US-10-425-115-59754 Sequence 59754, A
10	1058.5	37.2	323	4	US-10-369-493-5321 Sequence 5321, Ap
11	936	32.9	344	5	US-10-732-923-19208 Sequence 19208, A

12	919.5	32.3	317	5	US-10-732-923-19321 Sequence 19321, A
13	919.5	32.3	317	6	US-11-097-143-816 Sequence 816, Appl
14	840.5	29.5	311	5	US-10-732-923-19320 Sequence 19320, A
15	840.5	29.5	311	5	US-10-507-617-58 Sequence 58, Appl
16	840.5	29.5	311	6	US-11-097-143-27690 Sequence 27690, A
17	839.5	29.5	294	5	US-10-507-617-55 Sequence 55, Appl
18	839.5	29.5	311	5	US-10-732-923-19319 Sequence 19319, A
19	781	27.4	301	5	US-10-732-923-19326 Sequence 19326, A
20	781	27.4	301	5	US-10-745-237-168 Sequence 168, Appl
21	781	27.4	301	6	US-11-097-143-555 Sequence 555, Appl
22	608	21.4	309	4	US-10-437-963-154439 Sequence 154439, A
23	607	21.3	308	4	US-10-767-701-45989 Sequence 45989, A
24	603.5	21.2	344	4	US-10-425-114-47724 Sequence 47724, A
25	602.5	21.2	302	5	US-10-732-923-19256 Sequence 19256, A
26	602.5	21.2	302	5	US-10-732-923-19256 Sequence 19256, A
27	599	21.0	301	4	US-10-425-114-47829 Sequence 47829, A
28	598	21.0	302	5	US-10-424-599-220995 Sequence 220995, A
29	596	20.9	301	4	US-10-732-923-19255 Sequence 19255, A
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32	592	20.8	311	4	US-10-425-115-264201 Sequence 264201, A
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34	589	20.7	317	4	US-10-732-923-19241 Sequence 19241, A
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42	584.5	20.5	297	5	US-10-732-923-19247 Sequence 19247, A
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44	541.5	19.0	1796	5	US-10-424-599-217619 Sequence 217619, A
45	529	18.6	290	4	US-10-732-923-19283 Sequence 19283, A
					Sequence 302730, A

ALIGNMENTS

RESULT 1
US-10-408-765A-2204
; Sequence 2204, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Soim D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Marnett, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2204
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-2204

Alignment Scores:

Pred. No.: 5,64e-109
Score: 1603.00
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 56.3%
DB: 4
Length: 314
Matches: 314
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-09-888-264-2 (1-1503) x US-10-408-765A-2204 (1-314)

[illegible]

RESULT 2
US-10-408-765A-3015
Sequence 3015, Application US/10408765A
Publication No. US20040101874A1
GENERAL INFORMATION:
APPLICANT: Ghost, Sonmitra S.
APPLICANT: Fahy, Boia D.
APPLICANT: Zhang, Bing
APPLICANT: Gibson, Bradford W.

```

: APPLICANT: Taylor, Steven W.
: APPLICANT: Glenn, Gary M.
: APPLICANT: WATNOCK, Dale E.
: TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
: TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
: FILE REFERENCE: 660088.465
: CURRENT APPLICATION NUMBER: US/10/408,765A
: CURRENT FILING DATE: 2003-04-04
: NUMBER OF SEQ ID NOS: 3077
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 3015
: LENGTH: 314
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-408-765A-3015

Alignment Scores:
Pred. No.:      5,64e-109      Length:      314
Score:          1603.00        Matches:      314
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%    Mismatches:  0
Query Match:    56.3%          Indels:      0
DB:             4              Gaps:        0
US-09-888-264-2 (1-1503) x US-10-408-765A-3015 (1-314)

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Qy	232	CCCTCGACCTGTGTGAAGAACCGAGATGCAAGTTGAGCCGGGAAGGGCCAAAGACTCGAG	293
Dp	41	ProLeuAspLeuValLVpAsnAspMetGlnLeuSerGlyGlyGlnValAluValLeuThrArgGlu	60
Qy	292	TACAAAACCAAGCTTCATGACCTCCACCAAGTATCCTGAAGCGAAGAGCCGTGAGGGGCATT	351
Dp	61	TyLVeThrSePheHisValLeuThrSerLeuValSerLeuValSerValAGlyLeuArgGlyLe	80
Qy	352	TACACGAGGCTGTCGGCGGCGCTGGTGGGTGACAGGCACTACACACATACCCGCTTGGC	411
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Dp	101	ILeTyThrValLeuPheGlyLysArgLeuThrArgLVpAlaArgLVpThrProGlyPheLeu	120
Qy	472	CTGAAGGCTGTGATTTGGCATGACCGCAGAGTCCACTGTGCTTTTGGGAAACCAAGCC	531
Dp	121	LeuLVpAlaValILeGlyMetThrValAGlyValAlaThrGlyValAspValGlyThrProAla	140
Qy	532	GAAGTGGCTTATATCCGATGACTCCGATGAGCGCGGCTTCAGATGCAAGCGCCGTGGC	591
Dp	141	GIuValAlaLeuILeArgMetThrLVpAlaArgLVpArgLeuProAlaAspGlnAspArgGly	160
Qy	592	TACAAATATGTATTAAAGCCGCTGATTCGAATCAACCGGGAAGAGGTGTCTCACATG	651
Dp	161	TyLVpAsnValPheAsnAlaLeuILeArgILeThrArgLVpGlyGlyValLeuThrLeu	180
Qy	652	TGGCGGGGCTGATCCCTTACCAATGGCTGGGGCGTCGTCCGTCAATGGTCGCCAGCTGGC	711
Dp	181	TrpArgGlyCysILeProThrMetValArgValaValaValaAsnAlaAlaGlnLeuAla	200
Qy	712	TCTCAATCCCAATCCAAAGAGATTCTTACTGCACTCAGGCTACTTCTTGCAACATCTTG	771
Dp	201	SeTrLVeSerGlnSerLVeGlnPheLeuLeuAspSerGlyTyTrpHisSerAspAsnILeLeu	220
Qy	772	TGCACATTTGTGGCCAGCATGATCAGCGGTCTTGTCAACACTGTGCTGCATGCTGTG	831
Dp	221	CysHisLVpAspCysAlaSerMetILeSerGlyLeuValThrThrAlaAlaSerMetProVal	240

GenCore version 5.1.7
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Run on: February 1, 2006, 14:43:32 ; Search time 1.88877 Seconds
(without alignments)
1723.464 Million cell updates/sec

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 75621 seqs, 10829074 residues

Total number of hits satisfying chosen parameters: 151242

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-TRANS-human40.cdi -LIST=45 -DOCAUGEN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0
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-USER=US09888264_QCEN_1_1_10@runat_01022006_131849_15001 -NCPU=6 -ICPU=3
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	554	19.5	313	US-11-010-239-109	Sequence 109, App
2	438.5	15.4	307	US-11-019-711-87	Sequence 87, Appl
3	430.5	15.1	307	US-11-019-711-88	Sequence 88, Appl
4	415.5	14.6	307	US-11-019-711-91	Sequence 91, Appl
5	407	14.3	306	US-11-019-711-89	Sequence 89, Appl
6	400	14.0	306	US-11-019-711-90	Sequence 90, Appl
7	387.5	13.6	323	US-10-063-703-126	Sequence 126, App
8	387.5	13.6	323	US-11-102-240-126	Sequence 126, App
9	344.5	12.1	271	US-11-019-711-26	Sequence 26, Appl

10	232	8.1	475	6	US-10-055-877-301	Sequence 301, App
11	213	7.5	469	6	US-10-063-703-58	Sequence 58, Appl
12	213	7.5	469	7	US-11-102-240-58	Sequence 58, Appl
13	213	7.5	568	6	US-10-055-877-300	Sequence 300, App
14	210	7.4	366	6	US-10-055-877-302	Sequence 302, App
15	209	7.3	384	6	US-10-055-877-299	Sequence 299, App
16	201	7.1	468	6	US-10-055-877-101	Sequence 101, App
17	199	7.0	308	5	US-09-978-3608-423	Sequence 423, App
18	151	5.3	196	7	US-11-186-284-35	Sequence 35, Appl
19	150.5	5.3	843	7	US-11-129-104-89	Sequence 89, Appl
20	148.5	5.2	482	6	US-10-055-877-298	Sequence 98, App
21	143	5.0	96	7	US-11-019-711-92	Sequence 92, Appl
22	143	5.0	96	7	US-11-019-711-93	Sequence 93, Appl
23	131.5	4.6	1970	6	US-10-821-234-1641	Sequence 1641, App
24	129.5	4.5	1207	7	US-11-149-003-120	Sequence 20, Appl
25	129	4.5	2102	6	US-10-995-561-990	Sequence 990, App
26	129	4.5	2108	6	US-10-995-561-989	Sequence 989, App
27	129	4.5	2157	6	US-10-995-561-991	Sequence 991, App
28	126	4.4	1464	7	US-11-000-463-243	Sequence 243, App
29	126	4.4	1464	7	US-11-186-284-28	Sequence 28, Appl
30	126	4.4	1464	7	US-11-021-603-2	Sequence 2, Appl
31	126	4.4	1467	6	US-10-821-234-1096	Sequence 1096, App
32	125.5	4.4	602	6	US-10-453-372-1064	Sequence 1064, App
33	125.5	4.4	1192	7	US-11-149-003-18	Sequence 18, Appl
34	125.5	4.4	1593	7	US-11-149-003-4	Sequence 4, Appl
35	124.5	4.4	3714	6	US-10-995-561-1015	Sequence 1015, App
36	124	4.4	1251	7	US-11-149-003-16	Sequence 16, Appl
37	123	4.3	1236	7	US-11-080-991-68	Sequence 68, Appl
38	122.5	4.3	1466	7	US-11-186-284-33	Sequence 33, Appl
39	122.5	4.3	1477	7	US-11-149-003-8	Sequence 8, Appl
40	122.5	4.3	1535	7	US-11-149-003-14	Sequence 14, Appl
41	122.5	4.3	1570	7	US-11-149-003-12	Sequence 12, Appl
42	122	4.3	1454	7	US-11-109-157A-2	Sequence 2, Appl
43	122	4.3	1566	6	US-10-453-372-1190	Sequence 1190, App
44	122	4.3	1686	7	US-11-109-157A-1	Sequence 1, Appl
45	122	4.3	1767	6	US-10-995-561-911	Sequence 911, App

ALIGNMENTS

RESULT 1
US-11-010-239-109
Sequence 109, Application US/11010239
Publication No. US20060015970A1
GENERAL INFORMATION:
APPLICANT: Roger PENNELL
APPLICANT: Jack OKAMURO
APPLICANT: Richard SCHNEEBERGER
APPLICANT: YIwen PANG
APPLICANT: Shing KWOK
APPLICANT: Diane JOFUKU
APPLICANT: Edward A. KIEGLE
APPLICANT: Jonathan DONSON
APPLICANT: Nestor APPIYA
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY USEFUL FOR
FILE REFERENCE: MODIFYING PLANT CHARACTERISTICS
CURRENT APPLICATION NUMBER: US/11/010.239
CURRENT FILING DATE: 2004-12-09
PRIOR APPLICATION NUMBER: US 60/529,352
NUMBER OF SEQ ID NOS: 133
SOFTWARE: PatentIn version 3.3
SEQ ID NO 109
LENGTH: 313
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(313)
OTHER INFORMATION: 12395532_protein_ID_12395534
US-11-010-239-109


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DB 79 GCGCGGACAGGAGCCCGAGCGGAGGCAATTGATGTGGATGGGCGGACAGGAGTG 138
QY 131 CGGAGGCGGAGGATAGACGGGAGGCCGCTACCTCCCTAAGTCCGTCAAGTTCTGT 190
DB 139 CGGAGGCGGAGGATAGACGGGAGGCCGCTACCTCCCTAAGTCCGTCAAGTTCTGT 198
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QY 1211 AGCTTGCCCTGTGCTGTGCTGTGATTTCTGTGCTTGTGCTAATTTCTTGACAGGAG 1270
DB 1219 AGCTTGCCCTGTGCTGTGCTGTGATTTCTGTGCTTGTGCTAATTTCTTGACAGGAG 1278
QY 1271 CTGAAAACTTCTGAGATTTCTGGCTTCCCTGAGTTTAAATTACAGGCAACAG 1330
DB 1279 CTGAAAACTTCTGAGATTTCTGGCTTCCCTGAGTTTAAATTACAGGCAACAG 1338
QY 1331 ACAGCAGAAATCCCTTTGTGATGGGAAACCAAGGCAAGCTGAGGGGACAGGAGAG 1390
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RESULT 2
CR609603 1532 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CS0DC010Y007 of Neuroblastoma Cot
DEFINITION 25-normalized of Homo sapiens (human).
ACCESSION CR609603.1 GI:50490410
VERSION HTC; CDSLT_cDNA.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM

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REFERENCE
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
CONTACT : Feng Liang Email : fliang@life.uchicago.edu
REMARK http://fulllength.invitrogen.com/InvitrogenCorporation1600
Parade Avenue
Genoscope.
2 (bases 1 to 1532)

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REFERENCE
AUTHORS Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
TITLE BP 191 91006 BVR cedex - FRANCE (E-mail : segreif@genoscope.cns.fr)
JOURNAL - Web : www.genoscope.cns.fr)

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COMMENT
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
into the NotI and BclI V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

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ORIGIN

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Query Match 97.0%; Score 1457.4; DB 4; Length 1532;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1458; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1261 TTGCAAGGAGCTGAAAACTTCTGAGGATTTCTGGCTCCCTGAGTTTATGTTTACG 1320
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 QY 1501 AAA 1503
 Db 1501 AAA 1503

RESULT 2
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 LOCUS Homo sapiens clone 24408 2-oxoglutarate carrier protein mRNA,
 DEFINITION complete cds.
 ACCESSION AF070548
 VERSION AF070548.1 GI:3387910
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 SOURCE Homo sapiens (human)
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.

REFERENCE 1 (bases 1 to 1503)
 Andersson, B., Wentland, M.A., Ricafrente, J.Y., Liu, W., and Gibbs, R.A.
 A 'double adaptor' method for improved shotgun library construction
 JOURNAL Anal. Biochem. 236 (1), 107-113 (1996)
 PUBMED 8619474

REFERENCE 2 (bases 1 to 1503)
 Yu, W., Andersson, B., Worley, K.C., Muzny, D.M., Ding, Y., Liu, W.,
 Ricafrente, J.Y., Wentland, M.A., Lennon, G., and Gibbs, R.A.
 Large-scale concatenation cDNA sequencing
 JOURNAL Genome Res. 7 (4), 353-358 (1997)
 PUBMED 910174

REFERENCE 3 (bases 1 to 1503)
 Yu, W., and Gibbs, R.A.
 Direct Submission
 Submitted (05-JUN-1998) Molecular and Human Genetics, Baylor
 College of Medicine, One Baylor Plaza S930, Houston, TX 77030, USA
 JOURNAL Location/Qualifiers
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 source

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 ORIGIN

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapevt 1.0

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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ABA93092; 12-APR-2002 (first entry)

Human 2-oxoglutarate carrier (OGC) cDNA sequence AF070548 SEQ ID NO:2.

Human, 2-oxoglutarate carrier; OGC; uncoupling protein; UCP; gene;

immunopreventive; immunomodulator; vulnerability; cerebroprotective;

anorectic; obesity; cachexia; metabolic disorder; stroke; trauma; sepsis;

infection; ss.

Homo sapiens.

WO200198512-A2.

27-DEC-2001.

22-JUN-2001; 2001WO-US020020.

22-JUN-2000; 2000US-0213307P.

(GETH) GENENTECH INC.

Adams S, Yu XX;

WPI; 2002-130794/17.

Screening for compounds that affect uncoupling, useful for identifying

human 2-oxoglutarate carrier (OGC) agonists or antagonists for treating

obesity or cachexia, respectively, by analyzing the expression of human

OGC within the sample.

Example 1; Page 26; 53pp; English.

The present invention describes a method of screening for compounds that

affect uncoupling. The method comprises analysing the expression of a

human 2-oxoglutarate carrier (OGC) protein within the sample. OGC has

anorectic, immunomodulator, vulnerability, cerebroprotective and

CC immunosuppressive activities. The method is useful for screening
CC compounds that affect uncoupling, particularly OGC antagonists or
CC agonists. The OGC agonist is particularly useful for increasing the
CC metabolic rate in a mammal to treat obesity. The OGC antagonist is useful
CC for treating cachexia. The method is also useful for detecting and
CC treating metabolic disorders. Modulating the metabolic rate in a mammal
CC has a variety of therapeutic applications, including treatment of obesity
CC and the symptoms associated with stroke, trauma (e.g. burn trauma),
CC sepsis or infection. OGC is an uncoupling protein. The present sequence
CC represents a human OGC cDNA sequence used in the exemplification of the
CC present invention, which is that of the Genbank accession number AF070548
CC
CC
CC Sequence 1503 BP, 285 A, 451 C, 437 G, 330 T, 0 U, 0 Other;

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DT	12-FEB-2004 (first entry)
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DE	Human solute carrier family 25 member 11 coding sequence.
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KX	Energy homeostasis; mouse; metabolism; triglyceride; metabolic disease;
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Copyright (c) 1993 - 2006 Biocelebration Ltd.

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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Patent No. US20020103150A1
GENERAL INFORMATION:
APPLICANT: Adams, Sean
APPLICANT: Xu, Xiang Xian
TITLE OF INVENTION: CONTROL OF METABOLISM WITH COMPOSITIONS OF THE HUMAN 2-OXOGLUTARATE
FILE REFERENCE: 10466/35
CURRENT APPLICATION NUMBER: US/09/888,264
CURRENT FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: 60/213,307
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 1503
TYPE: DNA
ORGANISM: Homo sapiens; GenBank AF070548
US-09-888-264-2

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RESULT 2
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Sequence 12, Application US/10507617
Publication No. US20050119206A1
GENERAL INFORMATION:
APPLICANT: Eulenberg, Karsten
APPLICANT: Steuernagel, Arnd
APPLICANT: Haeder, Thomas
APPLICANT: Broemner, Guenter
TITLE OF INVENTION: CG8327, CG10823, CG18418, CG15862, CG3768, CG11447 and CG16750
TITLE OF INVENTION: Homologous Proteins Involved in the Regulation of Energy
FILE REFERENCE: 2823-651
CURRENT APPLICATION NUMBER: US/10/507,617
CURRENT FILING DATE: 2004-09-14
PRIOR APPLICATION NUMBER: PCT/EP03/02714
PRIOR FILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: EP 02 005 882.2
PRIOR FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: EP 002 006 012.5
PRIOR FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: EP 02 006 271.7
PRIOR FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: EP 02 006 810.2
PRIOR FILING DATE: 2002-03-25
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PatentIn version 3.2
SEQ ID NO 12
LENGTH: 1570
TYPE: DNA
ORGANISM: Homo sapiens
US-10-507-617-12

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QY	131	CCGGGGGCGGGAGGTAGACGGGAAAGGCCGGTACCTCCCTTAAGTCGGTCAAGTTCCGT	190	
Db	142	CCGGGGGCGGGAGGTAGACGGGAAAGGCCGGTACCTCCCTTAAGTCGGTCAAGTTCCGT	201	
QY	191	TTGGGGGCTTGCGCCGGGATGGGAGCTACAGTTTGTGTCCAGCCCTCGGACTGTGTGAAGA	250	
Db	202	TTTGGGGGCTTGCGCCGGGATGGGAGCTACAGTTTGTGTCCAGCCCTCGGACTGTGTGAAGA	261	
QY	251	ACCGGATGCAATTGAGCGGGGAAAGGGGCGAAGACTGCAAGATCAAAAACCAAGCTTCCATG	310	
Db	262	ACCGGATGCAATTGAGCGGGGAAAGGGGCGAAGACTGCAAGATCAAAAACCAAGCTTCCATG	321	
QY	311	CCCTCACCAGATCTCTTAAGGCGAAGGCCCTGAGAGGGGCAATTACACTGGGCTGTGGGCTG	370	
Db	322	CCCTCACCAGATCTCTTAAGGCGAAGGCCCTGAGAGGGGCAATTACACTGGGCTGTGGGCTG	381	

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 1, 2006, 20:32:32 ; Search time 732.559 Seconds
(without alignments)
10216.861 Million cell updates/sec

Title: US-09-888-264-1

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Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 333246308 residues

Total number of hits satisfying chosen parameters: 9993994

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	945	84.1	945	13	ADQ89939 Antagonis
6	874.6	77.9	1098	12	ADJ27261 Human TRI
7	874.6	77.9	2586	10	ADG30801 Human nov
8	802.6	71.5	1091	12	ADJ67689 Klf1C DNA
9	787.2	70.1	946	10	ADBS8443 Toxicity
10	787.2	70.1	946	12	ADP72899 Renal tox
11	787.2	70.1	946	13	ADV41249 Rat cardi
12	787.2	70.1	946	14	ADZ60768 Rat LOC64
13	701.8	62.5	1466	12	ADJ27252 Human TRI
14	609.6	54.3	947	13	ADN33186 Human tria
15	440.2	39.2	552	9	ACH23567 Human adu
16	362	32.2	418	9	ACH13741 Human adu
17	359	32.0	454	9	ACH14565 Human adu
18	356.6	31.8	1654	4	AB102383 Drosophila
19	337.4	30.0	2038	13	ACN43709 Human dia

C	20	337.4	30.0	2122	13	ACN43708 Human dia
C	21	337.4	30.0	2268	13	ACN43706 Human dia
C	22	314.6	28.0	3725	4	AB102382 Drosophila
C	23	308.6	27.5	1205	13	ADK51274 Plant ful
C	24	269.4	24.0	24741	11	ACN44542 Human gen
C	25	259.4	23.1	1398	14	ADY64719 S. manson
C	26	255.6	22.8	688	13	ADG51456 Novel can
C	27	254.6	22.7	1017	4	AB120299 Drosophila
C	28	254.6	22.7	3017	4	AB120298 Drosophila
C	29	248.2	22.1	906	4	AB102209 Drosophila
C	30	248.2	22.1	906	13	ADG89737 Antagonis
C	31	248.2	22.1	2906	4	AB102208 Drosophila
C	32	216	19.2	24127	11	ACN44540 Human gen
C	33	180.8	16.1	613	10	ADJ32951 Human mit
C	34	173.4	15.4	1866	3	AAAC33719 Human mac
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C	41	142.4	12.7	458	4	AD17748 Human mac
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ALIGNMENTS

RESULT 1
ID ABA93091 standard; cDNA; 1123 BP.

XX ABA93091;

DT 12-APR-2002 (first entry)

DE Human 2-oxoglutarate carrier (OGC) cDNA sequence NM_003562 SEQ ID NO:1.

XX Human; 2-oxoglutarate carrier; OGC; uncoupling protein; UCP; gene;

KW immunosuppressive; immunomodulator; vulnereary; cerebroprotective;

KW anorectic; Obesity; cachexia; metabolic disorder; stroke; trauma; sepsis;

KW infection; ss.

XX Homo sapiens.

OS WO200198512-A2.

PD 27-DEC-2001.

PP 22-JUN-2001; 2001WO-US020020.

PR 22-JUN-2000; 2000US-0213307P.

PA (GETH) GENENTECH INC.

PI Adams S, Yu XX;

DR WPI; 2002-130794/17.

PT Screening for compounds that affect uncoupling, useful for identifying human 2-oxoglutarate carrier (OGC) agonists or antagonists for treating obesity or cachexia, respectively, by analyzing the expression of human OGC within the sample.

PS Example 1; Page 26; 53pp; English.

CC The present invention describes a method of screening for compounds that affect uncoupling. The method comprises analysing the expression of a

CC human 2-oxoglutarate carrier (OGC) protein within the sample. OGC has anorectic, immunomodulator, vulnereary, cerebroprotective and

CC

CC immunosuppressive activities. The method is useful for screening
 CC compounds that affect uncoupling, particularly OGC antagonists or
 CC agonists. The OGC agonist is particularly useful for increasing the
 CC metabolic rate in a mammal to treat obesity. The OGC antagonist is useful
 CC for treating cachexia. The method is also useful for detecting and
 CC treating metabolic disorders. Modulating the metabolic rate in a mammal
 CC has a variety of therapeutic applications, including treatment of obesity
 CC and the symptoms associated with stroke, trauma (e.g. burn trauma),
 CC sepsis or infection. OGC is an uncoupling protein. The present sequence
 CC represents a human OGC cDNA sequence used in the exemplification of the
 CC present invention, which is that of the GenBank accession number
 CC NM_003562

XX Sequence 1123 BP; 229 A; 330 C; 332 G; 232 T; 0 U; 0 Other;

Query Match 100.0%; Score 1123; DB 6; Length 1123;

Best Local Similarity 100.0%; Pred. No. 3.1e-283; Mismatches 0; Gaps 0;

Matches 1123; Conservative 0; Indels 0; Gaps 0;

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 DB 1 CCGAGGGCCATTGATGCGATGCGCGGAGAGTGCCTGGGCGCGGATGAGACG 60

QY 61 GGAAGCCCGTACCTCCCTTAAGTCCGTCAGATTCTGTTGGGGGCTTGGCGGATGG 120
 DB 61 GGAAGCCCGTACCTCCCTTAAGTCCGTCAGATTCTGTTGGGGGCTTGGCGGATGG 120

QY 121 GAGCTACAGTTTGTTCAGACCCCTGGACCTGGAGAAAGAACCGGATGAGGCGGG 180
 DB 121 GAGCTACAGTTTGTTCAGACCCCTGGACCTGGAGAAAGAACCGGATGAGGCGGG 180

QY 181 AAGGGGCCAAGACTCGAGATACAAAACAGCTTCATGCTCCACAGATCTGTAAG 240
 DB 181 AAGGGGCCAAGACTCGAGATACAAAACAGCTTCATGCTCCACAGATCTGTAAG 240

QY 241 CAGAAGGCTGAGGGGCGATTATACATGCGCTGCGCTGCTGCTGCTGCTGCTGCT 300
 DB 241 CAGAAGGCTGAGGGGCGATTATACATGCGCTGCGCTGCTGCTGCTGCTGCTGCT 300

QY 301 ACACCACTACCGCGCTTGGCATATACCGTGCCTGTTGAGCGGCTGACCTGGGGCTGATG 360
 DB 301 ACACCACTACCGCGCTTGGCATATACCGTGCCTGTTGAGCGGCTGACCTGGGGCTGATG 360

QY 361 GTACTCCCGCTGCTTCTGCTGAGGCTGTGATTGGCATGACCGAGGTGCCACTGTG 420
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QY 421 CTTTGTGGGAACACGACCGGAAGTGTCTTATCCGATGACTGCCGATGCGCGCTTC 480
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QY 601 TCAATGCTGCGAGCTGCTCTTACTCCCAATCCAAAGTCTTATCTGAGCTAGGCT 660
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RESULT 2
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 ID AD162922 standard; cDNA; 1434 BP.

XX AD162922;
 XX 22-APR-2004 (first entry)

DE Human apoptosis-associated cDNA SEQ ID 365.
 XX

KW apoptosis; cell death; cytoskeletal; neuroprotective; immunosuppressive;
 KW antineuritic; antitachytic; dermatological; antiinflammatory;
 KW hepatotropic; virucide; neurotropic; anticonvulsant; antiparkinsonian;
 KW vasotrophic; cerebroprotective; antialcoholic; gene therapy; tumour;
 KW autoimmune disease; degenerative disease; viral infection; leukaemia;
 KW carcinoma; sarcoma; multiple sclerosis; rheumatoid arthritis; diabetes;
 KW lupus; hepatitis; influenza viruses; Alzheimer's disease;
 KW Huntington's disease; Parkinson's disease; reperfusion injury; stroke;
 KW alcoholic liver disease; human; gene; ss.

OS Homo sapiens.
 XX

PN MO2003058021-A2.
 XX

PD 17-UTL-2003.
 XX

PF 13-JAN-2003; 2003WC-EP000270.
 XX

PR 11-JAN-2002; 2002DE-01000856.
 XX

PA (XANT-) XANTOS BIOMEDICINE AG.
 XX

PI Koenig-Hoffman K, Kazinski M, Schaefer R, Keeper B;
 XX

DR MPI; 2003-542134/51.
 XX

XX Claim 1b; SEQ ID NO 365; 517bp; German.
 XX This invention describes novel nucleic acid molecules that are associated
 CC with apoptosis and encode a polypeptide and are derived from a normalised
 CC gene library (embryonic or liver) or clone collections, and the extent of
 CC apoptosis measured by cell death detection assay or the CPRG assay
 CC (measuring loss of membrane integrity). The products of the invention
 CC have cytoskeletal, neuroprotective, immunosuppressive, antineuritic,
 CC antitachytic, dermatological, antiinflammatory, hepatotropic, virucide,
 CC neurotropic, anticonvulsant, antiparkinsonian, vasotrophic.

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OY	661	ACTTCTGTGACCAACATCTGTGTGCCATTTCTGTGCCAGATGATCAGCGGCTTGTACCA	720
Db	661	ACTTCTGTGACCAACATCTGTGTGCCATTTCTGTGCCAGATGATCAGCGGCTTGTACCA	720
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VERSION	CQ725283.1		GI:42286140		
KEYWORDS					
SOURCE					
	Homo sapiens (human)				

ORGANISM	Human sapiens
ORGANISM	Human sapiens
REFERENCE	Kumariyola; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
TITLE	Hominidae; Homo.
JOURNAL	Venter, C.J., Adams, M.C., Li, P.W., and Myers, E.W.
FEATURES	Kits, such as nucleic acid arrays, compiling a majority of human exons or transcripts, for detecting expression and other uses thereof
FEATURES	Patent: WO 02068579-A 11217 06-SEP-2002;
FEATURES	PE Corporation (NY) (US)
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4	61 GGAAGCCCGGCTACCTCCCTTAAGTCCGTCAAGTTCCTGTTGGGAGGCTGAGCGGATAG 120
5	121 GAGCTACAGTTTTTGTGTCCAGCCCTCGACCTGTGTGAAGAACCGGATGCAATTGAGCGGG 180
6	121 GAGCTACAGTTTTTGTGTGTCCAGCCCTCGACCTGTGTGAAGAACCGGATGCAATTGAGCGGG 180
7	181 AAGGGGCGCAAGACTCGAGAGTCAAAACACAGCTCAATGCCCTCAACAGTATCCGAAAG 240
8	181 AAGGGGCGCAAGACTCGAGAGTCAAAACACAGCTCAATGCCCTCAACAGTATCCGAAAG 240
9	241 CAGAAGGCTGAGGGGCAATTACACTGGGCTGTGGGCTGGCTGGCTGGCTGGCTGGCTGGCT 300
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14	361 GTACTCCCGCTGGCTTCTGTGTGAAGGCTGTGATTTGGCATGACCGGAGTGCACCTGGT 420
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GenCore version 5.1.7
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	945	84.1	945	US-10-745-237-369	Sequence 369, App
5	802.6	71.5	1091	US-10-261-175A-5	Sequence 5, Appli
6	787.2	70.1	946	US-10-191-803-147	Sequence 147, App
7	787.2	70.1	946	US-10-764-420-492	Sequence 492, App
8	440.2	39.2	552	US-09-918-995-10779	Sequence 10779, A
9	362	32.2	418	US-09-918-995-953	Sequence 953, App
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12	314.6	28.0	3725	US-11-097-143-814	Sequence 814, App
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17	269.4	24.0	14943	US-10-741-600-17978	Sequence 17978, A
18	269.4	24.0	17149	US-10-741-600-17980	Sequence 17980, A
19	269.4	24.0	17441	US-10-087-192-1042	Sequence 1042, App
20	254.6	22.7	1017	US-11-097-143-27689	Sequence 27689, A
21	254.6	22.7	3017	US-11-097-143-27688	Sequence 27688, A
22	248.2	22.1	906	US-10-745-237-167	Sequence 167, App
23	248.2	22.1	906	US-11-097-143-554	Sequence 554, App

24	248.2	22.1	2906	10	US-11-097-143-553	Sequence 553, App
25	216	19.2	24127	5	US-10-087-192-1039	Sequence 1039, App
26	201.2	17.9	1350	7	US-10-437-963-23510	Sequence 23510, A
27	180	16.0	1572	8	US-10-425-115-118087	Sequence 118087, A
28	169.4	15.1	1898	7	US-10-425-114-6241	Sequence 6241, App
29	169.4	15.1	12201	7	US-10-424-599-133253	Sequence 133253, A
30	157	14.0	1578	7	US-10-424-599-133252	Sequence 133252, A
31	153.2	13.6	660	7	US-10-437-963-56406	Sequence 56406, A
32	149	13.3	747	7	US-10-425-114-4247	Sequence 4247, App
33	143.2	12.8	1414	8	US-10-425-115-30789	Sequence 30789, A
34	143	12.7	761	8	US-10-425-114-19049	Sequence 19049, A
35	143	12.7	761	8	US-10-425-115-118086	Sequence 118086, A
36	142.4	12.7	366	9	US-10-505-680-545	Sequence 545, App
37	142.2	12.7	1206	7	US-10-424-599-74777	Sequence 74777, A
38	138.4	12.3	1167	7	US-10-425-114-18168	Sequence 18168, A
39	138.4	12.3	1368	7	US-10-425-114-3304	Sequence 3304, App
40	138.4	12.3	1931	8	US-10-425-115-79538	Sequence 79538, A
41	136.8	12.2	1238	7	US-10-425-114-19387	Sequence 19387, A
42	135.8	12.1	816	6	US-10-369-493-27138	Sequence 27138, A
43	135.2	12.0	1477	7	US-10-425-114-26168	Sequence 26168, A
44	134.6	12.0	1493	7	US-10-424-599-78156	Sequence 78156, A
45	132	11.8	1406	7	US-10-260-238-4237	Sequence 4237, App

ALIGNMENTS

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US-09-888-264-1
Sequence 1, Application US/09888264
Patent No. US20020103150A1
GENERAL INFORMATION:
APPLICANT: Yu, Xiang Xian
TITLE OF INVENTION: CONTROL OF METABOLISM WITH COMPOSITIONS OF THE HUMAN 2-OXOGLOUTARATE.
FILE REFERENCE: 10466/35
CURRENT APPLICATION NUMBER: US/09/888, 264
CURRENT FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: 60/213,307
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1123
TYPE: DNA
ORGANISM: Homo sapiens; GenBank NM_003562
US-09-888-264-1

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121	GAGTACAGTTTGTCCAGCCCTGAGCCTGAGCCTGAGAACCGAGTGCAGTTGACGGGG	180							
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RESULT 2

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US-09-888-264-2
/ Sequence 2, Application US/09888264
/ Patent No. US20020103150A1
/ GENERAL INFORMATION:
/ APPLICANT: Adams, Sean
/ APPLICANT: Yu, Xiang Xian
/ TITLE OF INVENTION: CONTROL OF METABOLISM WITH COMPOSITIONS OF THE HUMAN 2-OXOGLUTARATE
/ FILE REFERENCE: 10466/35
/ CURRENT APPLICATION NUMBER: US/09/888,264
/ PRIOR FILING DATE: 2001-09-17
/ PRIOR APPLICATION NUMBER: 60/213,307
/ NUMBER OF SEQ ID NOS: 2
/ SOFTWARE: PatentIn version 3.1

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/ SEQ ID NO 2
/ LENGTH: 1503
/ TYPE: DNA
/ ORGANISM: Homo sapiens; GenBank AF070548
US-09-888-264-2
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Best Local Similarity 99.1%; Pred. No. 6,5e-289;
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GenCore version 5.1.7
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1604	73.5	314	4	US-10-408-765A-498 Sequence 498, App
2	1600	73.4	314	4	US-10-408-765A-2204 Sequence 2204, App
3	1600	73.4	314	4	US-10-408-765A-3015 Sequence 3015, App
4	1600	73.4	314	5	US-10-507-617-13 Sequence 13, Appl
5	1600	73.4	314	5	US-10-745-237-370 Sequence 370, Appl
6	1558	71.4	314	5	US-10-507-617-57 Sequence 57, Appl
7	1517	69.6	297	4	US-10-507-617-56 Sequence 56, Appl
8	1056	48.4	310	4	US-10-425-115-211662 Sequence 211662, A
9	1056	48.4	312	4	US-10-425-114-59754 Sequence 59754, A
10	1052	48.2	323	4	US-10-369-493-5321 Sequence 5321, App
11	926.5	42.5	344	5	US-10-732-923-19208 Sequence 19208, A

12	915.5	42.0	317	5	US-10-732-923-19321 Sequence 19321, A
13	915.5	42.0	317	6	US-11-097-143-816 Sequence 816, App
14	839.5	38.5	294	5	US-10-507-617-55 Sequence 55, Appl
15	839.5	38.5	311	5	US-10-732-923-19320 Sequence 19320, A
16	839.5	38.5	311	5	US-10-507-617-58 Sequence 58, Appl
17	839.5	38.5	311	6	US-11-097-143-27690 Sequence 27690, A
18	838.5	38.4	311	5	US-10-732-923-19319 Sequence 19319, A
19	782	35.9	301	5	US-10-732-923-19326 Sequence 19326, A
20	782	35.9	301	5	US-10-745-237-168 Sequence 168, App
21	782	35.9	301	6	US-11-097-143-555 Sequence 555, App
22	610	28.0	309	4	US-10-437-963-154439 Sequence 154439, A
23	607	27.8	308	4	US-10-767-701-45989 Sequence 45989, A
24	602.5	27.6	302	5	US-10-732-923-19256 Sequence 19256, A
25	602	27.6	304	4	US-10-425-114-47724 Sequence 47724, A
26	599	27.5	301	4	US-10-424-599-220995 Sequence 220995, A
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ALIGNMENTS

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; Sequence 498, Application US/10408765A
; Publication No. US20040101874A1
GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary W.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 498
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-498
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Best Local Similarity: 100.0% Indels: 0
Query Match: 73.5% Gaps: 0
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; Sequence 2204, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Brian D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.

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; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2204
; LENGTH: 314
; TYPE: PR
; ORGANISM: Homo sapiens
US-10-408-765A-2204

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Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 99.7% Mismatches: 0
Query Match: 73.4% Indels: 0
DB: 4 Gaps: 0

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US-09-888-264-1 (1-1123) x US-10-408-765A-2204 (1-314)

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QY 21 ATGGCGGCGAAGAGTGCAGGAGCGGAGGATGACGGAAGCCCGTACCTCCCT 80
Db 1 MetAlaAlaThrAlaSerAlaGlyAlaGlyGlyMetAspGlyProArgThrSerPro 20
QY 81 AAGTCGTCGAAGTTCCTGTTTGGGGGCTGGCCGGATGGGAGCTACAGTTTGTCCAG 140
Db 21 LysSerValLysPheLeuPheGlyGlyLeuAlaGlyMetGlyAlaThrValPheValGln 40
QY 141 CCCCTGAGCTGGTGAAGAACCGGATGACGATTGAGCGGGGAAGGGCCAAAGACTCAGAG 200
Db 41 ProLeuAspLeuValLysAsnArgMetGlnLeuSerGlyGlnGlyAlaLysThrArgGln 60
QY 201 TACAAAACCAAGCTTCATGCTCCACCAAGTATCTGAAGGACAGAGGCTGAGGGGCAATT 260
Db 61 TyrLysThrSerPheHisAlaLeuThrSerIleLeuLysAlaGlnGlyLeuArgGlyIle 80
QY 261 TACACTGGGCTGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 320
Db 161 TyrLysThrSerPheHisAlaLeuThrSerIleLeuLysAlaGlnGlyLeuArgGlyIle 180
QY 321 ATCTATACGCTGTGCTTTGAGCGCTGACTGGGGCTGATGATGATCCCTGGCTTTCTG 380
Db 101 IleTyrThrValLeuPheGlnArgLeuThrGlyAlaAspGlyThrProProGlyPheLeu 120
QY 381 CTGAAGGCTGTGATGGCATGACCGCAGCTGACCTGTGCTGTGGGAAACACAGCC 440
Db 121 LeuLysAlaValIleGlyMetThrAlaGlyAlaThrGlyAlaPheValGlyThrProAla 140
QY 441 GAAGTGGCTTTATCCGATGACTGCGGATGGCGGCTTCCAGCTGACCGCCGCTGGC 500
Db 141 GluValAlaLeuIleArgMetThrAlaAspGlyArgLeuProAlaAspGlnAlaGlyGly 160
QY 501 TACAAAATGTGTTTAAAGCGCTGATTCGATACCGGAGAGAGGGTGTCTCACAGCT 560
Db 201 SerTyrSerGlnSerIleArgGlnPheLeuAspSerGlyTyrPheSerAspAsnIleLeu 220
QY 561 TGGCGGGCTGATCCCTACCATGCTCGGAGCGCTGTGCTGATGCTGCTGCTGCTGCTG 620
Db 181 TrpArgGlyCysIleProThrMetAlaArgAlaValAlaValAsnAlaAlaGlnLeuAla 200
QY 621 TCTTACTCCCAATCCAAAGAGTTCTTACTGGAATCGAGCTTCTTCTGACACATCTTG 680
Db 201 SerTyrSerGlnSerIleArgGlnPheLeuAspSerGlyTyrPheSerAspAsnIleLeu 220
QY 681 TGCACCTTCTGTGCGACGATGATCAGCGGCTTGTGACACGCTGCTGCTGCTGCTGCTG 740
Db 221 CysHisPheCysAlaSerMetIleSerGlyLeuValThrThrAlaAlaSerMetProVal 240

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Db      22 pheValAsnGlyGlyAlaSerGlyMetLeuAlaThrCysValIleGlnProIleAspMet 41
QY      153 GTGAAGAACCGATGAGTGTAGCGGGGAAAGGGCCCAAGATCGAGAGTACAAACCAGC 212
Db      42 ValIyValIyValIleGlnLeu---GlyGlyGlySerAlaAlaThrValThrIys----- 58
QY      213 TTCATGACCCCTCACCAGTATCTGAAAGGAGAAAGCCCTGAGGGGCACTTACACTGGGCTG 272
Db      59 -----LysMetLeuAlaAsnGlyGlyIleGlySerPheThrIySerGlyLeu 73
QY      273 TCGGCTGGCTGTGCTGTGACGACCTTACACACATCCGCTTGGCATCTATACCG 332
Db      74 SerAlaGlyLeuLeuArg---AlaThrIyThrAlaArgLeuGlySerPheArgVal 92
QY      333 CTGTTGAGCGCCTGACTGGGGCT---GATGTACTCCCGCTGGCTTCTGTGAGAGGCT 389
Db      93 LeuThrAsnIyValAlaValGlyAlaAsnGlyGlyIleProLeuProLeuLeuGlnIyValAla 112
QY      390 GTGATTTGAGCATGACCCGAGGTGCGCACTGTGCTTTGTGGGAAACACCGAGTGGCT 449
Db      113 ValIleGlyLeuThrAlaGlyAlaIleGlyAlaSerAlaGlySerProAlaAspLeuAla 132
QY      450 CTATATCCGATGACTGCGCATGCGCGCTTCCAGCTGACAGCGCGCTGCTCAAAAAT 509
Db      133 LeuIleArgMetGlnIleAspSerThrLeuProAlaAlaGlnArgArgAsnIyIyValAsn 152
QY      510 GTGTTTAAGCGCCTGATTCGATCACCCGGGAAAGGGTGTCTCTCACTGCTGGCGGGC 569
Db      153 AlaPheHisAlaLeuIyArgIleValAlaAspGlyValIleuAlaLeuIyIySerGly 172
QY      570 TGCATCCATACATGCTGCGGCGCTGCTGTCATGCTGCGCAGCTGCGCTCTTCC 629
Db      173 AlaGlyProThrValValAlaGlyAlaMetSerLeuAsnMetGlyMetLeuAlaSerIyAsp 192
QY      630 CATCCAGAGAGTCTTACTGAGC-----TCAGGCTACTTCTCTGCAACAATCCTG 660
Db      193 GlnSerValGlnLeuPheArgAspIyLeuGlyAlaGlyIleuLeuSerThrMetLeu--- 211
QY      681 TGCCACTTCTGTGCTGACGATGACGCGGTCTGTGACCACTGCTGCTGCATGCTGTG 740
Db      212 -----GlyAlaSerAlaValSerGlyPheCysAlaSerAlaCysSerLeuProPhe 228
QY      741 GACATTGCCAAGACCCGATCCAGAACATGCGGATG---ATTGATGGAAAGCCGGAATAC 797
Db      229 AspIyValIySerThrGlnIleGlnIyMetGlnProAspAlaAsnGlyIySerIyProIy 248
QY      798 AAGAAGCGGCTGACGCTGCTTCAAGTGTCCGCTACAGAGGCTTCTTCACTGTG 857
Db      249 ThrGlySerLeuAspCysValMetIyThrLeuIySerGlyGlyProPheIySerPheIy 268
QY      858 AAGGCTTCACGCGCTACTATGCGCGCTGGGCGCCACACACGCTCTCACTTCATCTTC 917
Db      269 ThrGlyPheProValIyIyCysValArgIleGlyProHisValMetLeuThrIyPhe 288
QY      918 TTGAGACGATGAACAGGCTTACAG 944
Db      289 LeuAsnGlnIleGlnIySpheGlnIyIy 297

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; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 17621
; LENGTH: 313
; TYPE: PRF
; ORGANISM: Candida albicans
US-09-248-796A-17621

Alignment Scores:
Pred. No.: 4,44e-39 Length: 313
Score: 513.00 Matches: 111
Percent Similarity: 57.3% Conservative: 58
Best Local Similarity: 37.6% Mismatches: 108
Query Match: 23.5% Indels: 18
DB: 2 Gaps: 4

US-09-888-264-1 (1-1123) x US-09-248-796A-17621 (1-313)
QY      90 AAGTTCCTGTTGGGGGCTGGCCCGGAGATGGAGCTACAGTTTGTCCAGCCCTTGAC 149
Db      15 ArgPheIyIyGlyGlyAlaAlaSerMetAlaAlaCysValValThrIySProIleAsp 34
QY      150 CTGTGAGAGAACCGATGAGTGTGAGCGGGGAAAGGGCCCAAGCTCGAGAGTACAAACC 209
Db      35 LeuAlaIyValAlaArgLeuGlnThrAla-----ThrIySProIyGlnSer 49
QY      210 AGCTTCATGCCCCTCACCAGTATCTGAAAGGAGAAAGCCGTGAGGGCACTTACACTGG 269
Db      50 LeuLeuSerMetIleIyGlnIleIyThrIyGlyGlyValPheIyAlleIySerGly 69
QY      270 CTGTGCGCTGGCTGCTGCTGCTGACGCGCACTTACACACATCCGCTTGGCATCTATAC 329
Db      70 LeuThrAlaSerLeuLeuArgGlnAlaThrIySerThrAlaArgPheGlyIleIyGln 89
QY      330 GTGCTGTTGAGCGCTGACT-----GGGCTGATGGTACTCC 368
Db      90 PheLeuIyGlyGlnIyMetGlnSerIleAlaThrThrGlyGlyThrGlnGlnIyIy 109
QY      369 CCTGCTTCTGCTGAGGCTGTGATTTGACATGACCGAGTGCACCTGGTCTTGTG 428
Db      110 ProSerThrAlaValLeuLeuProMetSerMetIleAlaGlyAlaLeuGlyIyLeuVal 129
QY      429 GGAACACCGAGGAGTGGCTTATCCGATGACTGCGGATGCGGCTTCCAGCTGAC 488
Db      130 GlyAsnProSerAspValAlaAsnIleArgMetGlnAsnAspSerThrIySProIleAsn 149
QY      489 CAGCGCGCGGCTACAAAATGTTTAAAGCCCTGATTGCAATGACCGGGAGAGGGT 548
Db      150 GlnArgArgAsnIyArgAsnAlaPheAspGlyIleIyIyValIleCysGlnGlnGly 169
QY      549 GTCTTCACACTGTGGCGGGCTGTCATCCCTACCATGGCTCGGCGCTGTCTCAATGCT 608
Db      170 IleAsnSerLeuPheArgGlyLeuThrProAsnLeuIleArgIyValIleuMetThrAla 189
QY      609 GCCCAGCTGCGCTCTTACTCCCAATCCAGACGATTCTTACTGTGACTCAAGCTCTCT 668
Db      190 SerGlnValValIyThrIyAspIleAlaIySerIleLeuValAlaPheIleIleAsp 209
QY      669 ---GACAATCCTGTGCGCACTTGTGCGACATGATGACGCGCTTGTACCACTGCT 725
Db      210 ProSerIyIySerThrIySProIleAlaIleAlaIyLeuValAlaIleThr 229
QY      726 GCCTTCACACTGTGAGCATTTGCCAAGCCGGAATCCAGAACATGAGTATGATGAG 785
Db      230 ValCysSerProAlaAspValAlaIyIyThrArgIleMetAsnSerIyGlySerThrGly 249
QY      786 AAGCCGGAATACAGAACGCGCTGAC-----GTCTGTTCAAAAGTTGTC 830
Db      250 GlyGlySerGlyIyAspGlyValAlaGlyAsnAlaIleLeuIleLeuIySAsnAlaVal 269
QY      831 CGCTAGAGGCTTCTTACGCTGTGAGAGGCTTACGCGCGATATGCGCGCTGGG 890
Db      270 LyeHleGlyGlyIleGlyPheMetPheArgGlyIyIyLeuProSerPheIleArgLeuGly 289

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